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6, 2003, 12:46:55 ; Search time 28.5758 Seconds (without alignments) 573.557 Million cell updates/sec
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                           US-09-155-739-11
                                                                                                                                               January
                                                                                                                                               Run on:
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655 1 QVQLVQSGAEVKKPGASVKV.....NYGVYAMDYWGQGTLVTVSS 123 BLOSUM62 Gapop 10.0 , Gapext 0.5 Perfect score: Sequence: Scoring table:

908470 seqs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB : Maximum DB : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:
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/SIDS2/gggdata/geneseqg-emb1,AA1985.DAT:\*
/SIDS2/gggdata/geneseqg-emb2,AA1985.DAT:\* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT: A\_Geneseq\_101002:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Humanized VLA-4 an Humanised alpha-4 Humanised alpha-4 Humanised alpha-4 Mouse anti-VLA-4 a Mouse VLA-4 antibo Alpha-4 integrin m Heavy chain variab Humanised antibody A fusion of single
ID	AAR81323 AAR81333 AAR22428 AAW22413 AAR81330 AAR81327 AAW32410 AAW4124 AAW409034
g	116 118 118 118 123 223
% Query Match Length DB I	123 142 142 123 123 140 120 120
% Query Match	100.0 100.0 98.9 84.3 84.3 83.1 79.9 79.9
Score	655 655 655 655 655 655 655 655 655 655
Result No.	11 4 4 7 6 9 9 10

New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating inflammatory disease.

WPI; 1995-269276/35

	Humanised ATR-5 H Humanised anti-CDI MOUSE and human ch Human monoclonal a
720000000000000000000000000000000000000	AAB74981 AAR47491 ABB05993 ABB05997
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1121 1151 1164 1176 1176 1176 1176 1176 1176 117	44 44 45
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## ALIGNMENTS

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Humanized antibody; leukocyte adhesion molecule; {\it VLA-4}; therapeutic; antibody engineering.
                                                                  Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
                                                                                                                                                                                                              Saldanha J;
                AAR81323 standard; Protein; 123 AA.
                                                                                                                                                                                                             Leger OJ,
                                                                                                                                                                                             (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                            95WO-US01219.
                                                                                                                                                                            94US-0186269
                                                 02-APR-1996 (first entry)
                                                                                                                                                                                                              Bendig MM, Jones TS,
                                                                                                            Mus musculus.
                                                                                                                            WO9519790-A1.
                                                                                                                                                             25-JAN-1995;
                                                                                                                                                                            25-JAN-1994;
                                                                                                                                            27-JUL-1995.
                                 AAR81323;
RESULT 1
        AAR81323
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                           The sequence encodes the mouse antibody 21.6 heavy chain variable region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned CDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ9985-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids LA5, LBS and LG9 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DPKFQGRVTITADISASTAYMELSSLRSEDIAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used for inhibiting adhesion of a leukocyte to an endothelial cell and for treating inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for action of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human VLA-4 reshaped antibody 21.6 light heavy variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 655; DB 16; Length 123; 100.0%; Pred. No. 6.6e-53; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "complementarity determining region 1"
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132..142
/note="framework region 4"
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Claim 11; Page 69; 105pp; English.
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Best Local Similarity 100.0
Matches 123; Conservative
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chain variable region against leukkocyte adhesion molecule VLA.4.

Cloned cDNA sequences of mouse 21.6 VH (AAQ99892) and VL (AAQ9889)

regions are linked to human constant regions in the construction
of a humanized antibody against VLA.4. The 5' and 3' ends of the
mouse cDNAs are modified using PCR primers (AAQ99895-98) and then
subcloned into mammalian cell expression vectors containing human
kappa or gamma-1 constant regions. In the humanized heavy chain,
amino acids H27, H28, H29, H30, H44 nd H71 in the human HC VR framework are replaced by the amino acid present in the equivalent
position of the mouse 21.6 Ig H chain. Plasmids encoding the
chimeric antibodies are transfected into COS cells. The humanized
antibodies can be used to inhibit adhesion of a leukocyte to an
endothelial cell and to treat inflammatory diseases such as multiple
sclerosis. They can also be used in the treatment of stroke,
crebral traumas, meningitis or encephalitis. The antibodies can
also be used for detecting VLA-4, for affinity purification or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DPKFQGRVTITADISASTAYMELSSLRSEDIAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents the human reshaped antibody 21.6 heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 655; DB 16; Length 142; 100.0%; Pred. No. 7.8e-53; 1ve 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanised alpha-4 integrin antibody 21.6 VL version Ha.
                                                                                                                                                                                                                                                                                                                                                               Leger OJ, Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 11; 105pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inflammatory disease.
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W09519790-A1.
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                                                                       27-JUL-1995.
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atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                  Location/Qualifiers
                                                                                                                                                                                                                                                                  Example 6; Fig 11; 107pp; English.
                                                                                                                                                                                                                  (ATHE-) ATHENA NEUROSCIENCES INC.
                                          label= Leader
                                                                                                                /label= CDR2
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/label= FR2
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                                                                                                                          86..117
                                                                                                       /note=
              Chimeric Mus musculus;
Chimeric Homo sapiens;
                                                                                                                                                                                                                                     WPI; 1997-297879/27.
                        Chimeric synthetic.
                                                                                                                                                                                                                                          N-PSDB; AAT74789
                                                                                                                                                                                               21-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- CDR3 /note= "21.6 complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "21.6 complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "21.6 complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= FR4
/note= "21/28'CL framework region 4"
                                                                                                                                                                                                                                                                                                           /note= "21/28'CL framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "21/28'CL framework region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "21/28'CL framework region 2"
                                                                                                                                                         /label= Mat_protein
/note= "VH version Ha (Claim 25)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "21.6 complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "21.6 complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "21/28'CL Arg-72 is substd. by Ala of mouse 21.6 VL, important in supporting the CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "21/28'CL residues 27-30 are replaced by those of MAD 21.6, involved in antigen
                                            ö
    Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "21/28'CL framework region 1" 17..30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113..123
|Jabel= FR4
|note= "21/28'CL framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "21/28'CL framework region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "21/28'CL framework region 2"
100.0%; Score 655; DB 18; ilarity 100.0%; Pred. No. 7.8e-53; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanised alpha-4 integrin antibody 21.6 VH Ha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         AAW22413 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50..66
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67..98
/label= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric Mus musculus;
Chimeric Homo sapiens;
Chimeric synthetic.
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9718838-A1
                                                                                                                                                                                                                                                           121 VSS 123
                                                                                                                                                                                                                                                                                                   140 VSS 142
                                          Matches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW22413;
    Query Match
Best Local S
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us-09-155-739-11.rag

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Query Match 84.3%; Score 552; DB 16; Length 123; Best Local Similarity 82.9%; Pred. No. 2e-43; Matches 102; Conservative 11; Mismatches 10; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This polypeptide, designated Ha, comprises the heavy chain variable region (VH) of a humanised alpha-4 integrin antibody 21.6. It is composed of complementarity determining regions (CDRs) from the VH region (see AAW22410) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human 21/28 CL framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate fragments of mouse and human DNA sequences. The humanised 21.6 VL (see AAW22412) can be used to produce a claimed humanised 21.6 vL (see AAW22412) can be used manufacture of a medicament for treating asthma, a histosoclarosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic; antibody engineering.
                                                                                                                                                                                                                                                                                                      AIDS, dementia, diabetes, inflammatory bowel disease, Theumatoid arthritis, transplant rejection, graft versus host disease, theumatoid metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin generating idiotypic antibodes. It is also useful for generating idiotypic antibodies. The humanised antibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                              Uses of humanised alpha-4 integrin antibody - for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                98.9%; Score 648; DB 18; Length 123; nilarity 99.2%; Pred. No. 2.9e-52; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
                                                                                 Saldanha J, Yednock TA;
                                                                                                                                           asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR81330 standard; Protein; 123 AA.
                                                                                   Leger OJ,
                                                         (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                 Claim 25; Fig 7; 107pp; English.
             96WO-US18807
                                   95us-0561521
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/label= FR1
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                                                                                 Jones ST,
                                                                                                       WPI; 1997-297879/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         123 AA;
             21-NOV-1996;
                                  21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 122;
                                                                                Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Region
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The sequence represents the mouse anti-VLA-4 antibody 21.6 heavy chain variable region (without signal sequence). Cloned cDNA CDR sequences of mouse 21.6 variable light and variable heavy regions are linked to human constant framework regions of the REI antibody for the light chain and attibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ9895-98) and then subcloned into constant regions. In the humanized light chain, amino acids L45, L49, CC mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, CC L58 and L69 in the human kappa LCVR framework are replaced by the antino ccide present in the equivalent position of the mouse 21.6 Ig light chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a smultiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningtis or encephaltis. The antibodies can also be used to used for detecting VLA-4, for affinity purification or for generating
                                                                                                                                  /note= "mouse heavy chain variable complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "mouse heavy chain variable complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "mouse heavy light chain variable framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "mouse heavy chain variable complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                   /note= "mouse heavy chain variable framework region 2"
/note= "mouse heavy chain variable framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "mouse heavy chain variable framework
                                                                                                                                                                               determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leger OJ, Saldanha J;
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                                        region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region 4"
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                                                                                                    /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                           'label= CDR2
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                                                                                                                                                                                                                                                  /label= FR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-269276/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9519790-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-1994;
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1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

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                                               The sequence represents the mouse antibody 21.6 heavy chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VH and VL (see AAQ99889) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5 and 3 ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1
Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New humanised antibodies against VIA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                  "complementarity determining region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                    69..85 /note= "complementarity determining region
                                                                                                                                                                                                                                Mouse VLA-4 antibody 21.6 light heavy variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "framework region 3"
                                                                                                                                                                                                                                                                                                                                                            "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                        /note= "framework region 2"
                                                                                                                                                                                                                                                                                                                                     "signal peptide"
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                              AAR81327 standard; Protein; 140 AA.
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                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                       'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
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                                                                                                                                                                                                                                                                    antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-269276/35.
N-PSDB; AAQ99892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9519790-A1
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                                                                              VSS 123
                                                                                                    VSS 123
                                                                                                                                                                                                                                                                                          Aus musculus
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                                                                                                                                                                                                          23-MAR-1996
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                                                                                                                                                                                                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
constant regions. In the humanized heavy chain, amino acids H27, H28, H29, H30, H44 nd H71 in the human HC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig H chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "complementarity determining region 2"
                                                                                                                                                                                                                                  menigitis or encephalitis. The antibodies can also be used detecting VLA-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                    83.1%; Score 544; DB 16;
82.6%; Pred. No. 1.3e-42;
ive 11; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "framework region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-4 integrin mouse MAb 21.6 VH region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= Leader
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/label- FR4
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/label= CDR1
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/label= FR2
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/label= C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                               anti-idiotype antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                140 AA;
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                                                                                                                                                                                                                                                                                                                                                                Sequence
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Matches
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118 VSS 120
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                                                                                                                                        11-DEC-1997
  Synthetic.
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                                    Region
                                                           Region
                                                                                Region
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                                                                                                                                                                                                                                               This polypeptide comprises the heavy chain variable region (VH) of mouse anti-alpha-4 integrin monoclonal antibody 21.6. The complementarity determining regions (CDRs) of the 21.6 VH can be incorporated into a human 21/28'CL framework to produce a claimed humanised 21.6 VH (see AAW22413) and a claimed humanised 21.6 rantibody that is used in the manufacture of a medicament for treating a disease selected from asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, mayocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin for use as a vaccine or an immunogen. It is also useful for for use as a vaccine cranimodies. The humanised antibodies of the invention have a half-life in the human circulation essentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heavy chain; variable region; murine; mouse; human; cancer antigen;
antibody; humanised; NR-LU-13; NRX451; cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heavy chain variable region of humanised NR-LU-13 antibody NRX451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                             Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 140;
                                                                                                                                     Leger OJ, Saldanha J, Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.1%; Score 544; DB 18;
82.6%; Pred. No. 1.3e-42;
tive 11; Mismatches 10;
/note= "framework region 4"
                                                                                                                                                                                                                            Claim 18; Page 69-70; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW44124 standard; Protein; 120 AA.
                                                                                                                (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                          95US-0561521.
                                                                  96WO-US18807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 100; Conservative
                                                                                                                                    Bendig MM, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                          WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 AA;
                                                                                                                                                                        N-PSDB; AAT74760.
                     WO9718838-A1
                                                                  21-NOV-1996;
                                                                                         21-NOV-1995;
                                            29-MAY-1997
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61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                novel humanised Ab (hAb) binds the antigen bound by NR-LU-13. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised antibody binds same human cancer antigen as antibody NR-LU-13 - useful for pre-targeting methods, conventional antibody therapy and immunodiagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the heavy chain variable region of the humanised murine anti-human cancer antigen antibody (Ab) NR-LU-13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hAb, specifically NRX451, or its conjugates can be used for the manufacture of a diagnostic or medicament for cancer diagnosis or treatment. The hAb has reduced immunogenicity and toxicity in humans, but retains the ability to bind the NR-LU-13 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.9%; Score 523.5; DB 19; Length 120; Best Local Similarity 82.9%; Pred. No. 8.3e-41; Matches 102; Conservative 8; Mismatches 10; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pedersen JT;
                                                                                                                  /note= "complementarity determining region 2" 99..109
                                                                                                                                                                                     /note= "complementarity determining region 3"
                                                     /note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised antibody NRX451 heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mallet RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hylarides MD,
Location/Qualifiers
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Rees AR, Renojm, Searle SMJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 960S-0660362
                                                                                                                                                                                                                                                                                                                                                                                  97WO-US10074
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the humanised antibody NRX 451 (or an antigenbinding fragment), in which the murine parent antibody is ATCC CRL-12360 (also known as NU-LU-13 which targets a 40 kilodalton glycoprotein expressed by many carcinomas) and which comprises the light chain variable region appearing as AAU79033 and the heavy chain variable region appearing as AAU79033 and the heavy chain variable region appearing as AAU79033 and the heavy chain variable region appearing as AAU79033 and the heavy chain variable region appearing as AAU79034 antibody may be administered to treat cancers and use to detect the presence of the antigen in clinical samples. The antibody is a humanised antibody derived from NR-LU-13 antigen. The antibody but retains the ability to bind the NR-LU-13 antigen. The antibody elither does not possess N-linked glycosylation or its N-linked lummunogenicity or toxicity. The present sequence represents the heavy chain variable region of humanised antibody of the invention, NRX451.
                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised antibody NRX-451, which is derived from ATCC CRL-12360, but which has reduced immunogenicity or toxicity, useful for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DLSFQGRVTITADTSINTAYMELSSLRSDDTAVYYCSREVL---TGTWSLDYWGQGTLVT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYMHWVRQAPGQGLQWMGRIDPANGNTKC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23; Length 120;
                                                                                                                                                                                                                                                                                                          Searle SMJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptavidin; tumour cell; cancer; adenocarcinoma; hematological malignancy; huNR-LU-10; EGP40; EPCAM
                                                                                                                                                                                                                                                                                                          Hylarides MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.9%; Score 523.5; DB 2
82.9%; Pred. No. 8.3e-41;
live 8; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A fusion of single chain antibody/streptavidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB30693 standard; Protein; 431 AA
                                                                                                                                                                                                                                                                                                        Reno JM, Mallett RW,
Pedersen JT, Rees AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 4; 53pp; English.
                                                                                                                                                               97US-0871488.
                                                                                                                                                                                                             96US-0660362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                          Graves SS, Reno JM,
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-314754/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                            (NEOR-) NEORX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reating cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 AA;
Homo sapiens.
Synthetic.
                                                                  US6358710-B1
                                                                                                                                                                                                             17-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 VSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-APR-2001
                                                                                                                19-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                   denry AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB30693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB30693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
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The present sequence encodes a fusion of the single chain antibody bunk-LU-10 and streptavidin. The antibody binds the antigen EGP40 or EPCAM. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a first nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter, and a cloning site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a first nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer, e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    presence or absence of, or treating, a target site within a mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reno JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with cancer, e.g. adenocarcinomas -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.9%; Score 523.5; DB 22; Length 431; 82.9%; Pred. No. 3.4e-40;
                                                                                                                                                                                                                                                                                                                                                                                     Sanderson JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human/murine chimeric antibody HEF-RVL-M21g(gamma)1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                 Lin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     Schultz JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR76681 standard; Protein; 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 10; 100pp; English
                                                                                                                                      05-JUN-2000; 2000WO-US15595.
                                                                                                                                                                                                       99US-0137900.
99US-0168976.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Goshorn SC, Graves SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-091213/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sest Local Similarity
                                                                                                                                                                                                                                                                                                                (NEOR-) NEORX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAC86562
WO200075333-A1.
                                                                                                                                                                                                           07-JUN-1999;
                                                                                                                                                                                                                                           03-DEC-1999;
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                                                                    L4 - DEC - 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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The present sequence is a fragment of the chimaeric human/murine monoclonal antibody (MAb) ONS-M21. The MAb was prepd. by combining light and heavy variable region DNA, from a murine anti-human myeloblastoma cell MAb, with human light and heavy constant region sequences, respectively to produce chimaeric human/murine light and heavy chain DNA mols. A recombinant vector for the expression of the heavy and light chain DNA mols. was prepd., and used to transform a host cell. The host cell was then cultured, and the expression prods. of the heavy and light chain outlands. Sepd. and connected with a peptide linker to produce a single stranded Fv region. The reshaped Fv region has low human antigenicity, and is therefore expected to be useful as an agent for the diagnosis and treatment of cerebral tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                           Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-M21-g(gamma)1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reshaped anti-human myeloblastoma cell human antibody - has low human antigenicity, and is therefore useful for diagnosis and treatment of cerebral tumours, e.g. myeloblastoma
                                                                                            Murine; human; myeloblastoma; chimaera; monoclonal antibody; chimera; single stranded Fv region; low human antigenicity; diagnosis; treatment; cerebral tumour; reshaped.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.8%; Score 523; DB 17;
83.7%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Pages 38-39; 45pp; Japanese.
                                                                                                                                                                                                              ...19
'label = sig_peptide
                                                                                                                                                                                                                                                20..136
/label= mat_peptide
                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                69..85
/label= CDR_2
                                                                                                                                                                                                                                                                                 50..54
/label= CDR_1
                                                                                                                                                                                                                                                                                                                                              118..125
/label= CDR_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94JP-0285057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94JP-0252166.
93JP-0291078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHUS ) CHUGAI PHARM CO LTD.
                               09-DEC-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-358509/36.
N-PSDB; AAT38653.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g. myeloblastoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 136 AA;
                                                                                                                                                                                                                                                                                                                                                                                               JP08169900-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-1996
                                                                                                                                                               Synthetic.
AAW04396;
                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                 Region
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                                                                                                                                                                                                                                                                                                                                                  Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ94539 encodes AAR76681 the human/murine chimeric antibody HEF-YL-M219(gamma). The antibody is reactive with human medulloblastoma (a brain tumour) cells. The chimeric antibody can be used in the diagnosis and treatment of this disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reconstituted antibody against human medullo:blastoma cells - contains high proportion of human antibody origin and has low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.8%; Score 523; DB 16; Length 136; illarity 83.7%; Pred. No. 1.1e-40; Conservative 4; Mismatches 10; Indels
            Human; murine; chimeric antibody; HEF-RVL-M21g(gamma)1;
                            medulloblastoma; brain tumour; treatment; diagnosis.
                                                                                           Location/Qualifiers
                                                                                                                          /label= sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohtomo T, Sato K, Tsuchiya M;
                                                                                                                                                                                                                                          70..86
/label= CDR 2
87..118
/label= FR 3
                                                                                                                                                                                           /label= CDR 1
                                                                                                                                                                                                                                                                                                                             CDR 3
                                                                                                                                                                                                         56..59
/label= FR 2
                                                                                                                                            20..50
/label= FR 1
                                                                                                                                                                                                                                                                                                                                           127..136
/label= FR 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                              94WO-JP01763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93JP-0291078
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                                                                                                                                                                                                                                                                                                         119..126
/label= Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-200347/26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ94539.
                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 VSS 123
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                                                                                                         Peptide
                                                                                                                                          Peptide
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                 TP08169900-A
                                                                                                                                                                                                                                                                                                                                 18-OCT-1994;
19-NOV-1993;
        VSS 123
                       137 VSS 139
                                                                                                                                                                                                                                                                                                                 18-NOV-1994;
                                                                                                                                                                                                                                                                                                 02-JUL-1996
                                                                                                                                                                 Synthetic
                                                                                AAW04397;
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       121
                                                RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pSCFVT7-hM21; human; ONS-M21 antibody; chimeric protein; medulloblastoma; brain tumour; treatment; diagnosis; Fv fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ94548 is the plasmid pSCFVT7-hM21, which encodes AAR76682 the human antibody ONS-M21 Fv fragment. The plasmid was used in the construction of an expression vector, contg. cDNA encoding a human/murine chimmeric antibody, reactive with human medulloblastoma (a brain tumour) cells. The chimeric antibody can be used in the diagnosis and treatment of this disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
9
                                                                                                                                                                                                                                                                                                                                                                                         cells -
has low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Reconstituted antibody against human medullo:blastoma contains high proportion of human antibody origin and antigenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.8%; Score 523; DB 16;
83.7%; Pred. No. 2.2e-40;
ive 4; Mismatches 10;
                                                                                                                                                                                                "heavy variable region"
                                                                                                                                                                                                                                "light variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 35; Pages 98-99; 120pp; Japanese.
                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                /label= sig_peptide
                                                       AAR76682 standard; Protein; 269 AA.
                                                                                                        Human ONS-M21 antibody Fv fragment.
                                                                                                                                                                                                                "linker"
                                                                                                                                                                                                                                                                                                                                                 Ohtomo T, Sato K, Tsuchiya M;
                                                                                                                                                                                                                                                 /note= "FLAG"
                                                                                                                                                                                                                                                                                                  94WO-JP01763.
                                                                                                                                                                                                                                                                                                                93JP-0291078
                                                                                                                                                                                                                                                                                                                                 CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.77
Matches 103; Conservative
                                                                                                                                                                                                                        155..269
/note= "1
262..269
                                                                                                                                                                                                        140..154
                                                                                                                                                                                         23..139
                                                                                                                                                                                                                  /note=
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                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-200347/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 AA;
                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ94548.
          134 VSS 136
                                                                                       18-JAN-1996
                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                 19-OCT-1994;
                                                                                                                                                                                                                                                                                                                .9-NOV-1993;
121 VSS 123
                                                                                                                                                                                                                                                                 W09514041-A1
                                                                                                                                                                                                                                                                                 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                       AAR76682;
                                                                                                                                                                       Peptide
                                                                                                                                                                                       Region
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The present sequence is a scFv fragment from the chimaeric human/murine monoclonal antibody (MAb) ONS-M21. The MAb was prepd by combining light and heavy variable region DNA, from a murine anti-human myeloblastoma cell MAb, with human light and heavy constant region sequences, respectively to produce chimaeric human/murine light and heavy chain DNA mols. A recombinant vector of for the expression of the heavy and light chain DNA mols. was prepd., and used to transform a host cell. The host cell was then cultured, and the expression prods. of the heavy and light chain DNA mols. sepd. and connected with a peptide linker to produce a single stranded Fv region. The reshaped Fv region has low human antigenicity, and is therefore expected to be useful as an agent of the diagnosis and treatment of cerebral tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reshaped anti-human myeloblastoma cell human antibody - has low
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treatment of cerebral tumours, e.g. myeloblastoma
                                                                                                                                                                                                                                                                                                 Murine; human; myeloblastoma; chimaera; monoclonal antibody; chimera; single stranded Fv region; low human antigenicity; diagnosis; treatment; cerebral tumour; reshaped.
                                                                                                                                                                                                                                 Chimaeric human/murine MAb ONS-M21 scFv fragment.
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140..154
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262..269
/label= FLAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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|abel= sig_peptide
AAW04397 standard; Protein; 269 AA.
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155..261
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93JP-0291078.
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Length 269;

Score 523; DB 17; Pred. No. 2.2e-40;

79.88; 83.78; us-09-155-739-11.rag

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                                                                                                                        DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
     Gaps
                                                     23 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWYRQAPGQGLEWMGRIDPADGNTKY 82
                                   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for treating inflammatory diseases such as multiple sclerosis. Tracan also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                           Humanized VLA-4 antibody 21.6 heavy chain variable region, Hc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
 10; Indels
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 Mismatches
                                                                                                                                                                                                                                                                                                   AAR81325 standard; Protein; 119 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leger OJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody engineering.
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137 VSS 139
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Score 515; DB 16; Length 119; Pred. No. 5e-40;

78.6%; 82.9%;

Best Local Similarity

Query Match

Search completed: January 6, 2003, 13:15:18 Job time: 29.5758 secs

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January 6, 2003, 13:13:21; Search time 10.1879 Seconds (without alignments) 355.228 Million cell updates/sec
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                                                                                                                                                                                                                                                     US-09-155-739-11
655
1 QVQLVQSGAEVKKPGASVKV......NYGVYAMDYWGQGTLVTVSS 123
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                       262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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nd is derived by analysis of the total score distribution. SUMMARIES

	Description	Sequence 11, Appl	Sequence 11,	Sequence 17,	7 Sequence 17,	6	6	4	Sequence 4,	Sequence 19,	Sequence 132,	Sequence 99,	Sequence 109,	13, 7	3 Sequence 13,	12,	Sequence 12,	44,	44 Sequence 44,	Sequence 10,	0 Sequence 10,	17 Sequence 17,	14 Sequence 14,	Sequence 17,	41,	B Sequence 8,		59
SUMMARIES	ID	US-08-561-521-11	r-0895-	US-08-561-521-17	PCT-US95-01219-1	US-08-561-521-9	ī	US-08-561-521-4	PCT-US95-01219-4	US-08-871-488A-1	US-08-646-265A-132	US-08-646-265A-99	US-08-646-265A-109	-	PCT-US95-01219-1	$\overline{}$	PCT-US95-01219-1	4	PCT-US95-01219-4	US-08-561-521-10	PCT-US95-01219-1	US-08-290-592E-1	PCT-US95-10053-1	PCT-US96-09448-17	₹	US-08-232-081B-6	US-09-025-769B-3	US-09-025-769B-5
	Length DB	123 2		142 2					140 5	120 4	117 4	136 4	269 4				119 5		125	119		117	117	117			120 4	
æ	Query Match	100.0	100.0	100.0	100.0	84.3	84.3	83.1	83.1	79.9	79.8	79.8	79.8	78.6	78.6	78.2	78.2	77.1	77.1	75.6	75.6	75.1	75.1	75.1	75.1	75.0	74.7	74.7
	Score	655	655	655	655	552	552	544	544	523.5	523	523	523	515	515	512	512	202	202	495	495	492	492	492	The same		489.5	489.5
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0; Gaps

Length 123; Indels

Query Match 100.0%; Score 655; DB 2; Best Local Similarity 100.0%; Pred. No. 1.4e-58; Matches 123; Conservative 0; Mismatches 0;

Appl Appl Appl Appl Appl Appl Appl Appl	
63, 11112, 1112, 1112, 1112, 1112, 1112, 112,	
sednence sed	Leukocyte ew 2000
US-08-836-561-63 US-08-137-117D-112 US-08-253-877-2-19 US-08-253-877-2-19 US-08-523-877-2-19 US-08-603-024-18 US-08-964-690-23 US-09-301-593-41 US-09-301-593-41 US-09-481-882-882-53 US-08-482-882-53 US-08-487-113D-53 US-08-487-113D-53 US-08-487-113D-53 US-08-487-113D-53 US-08-487-113D-53 US-08-487-113D-53 US-08-487-113D-53 US-08-487-113D-53 US-08-487-113D-53	ALIGNMENTS  d Antibodies Against Molecule VLA-4  wnsend Khourie and Cr Steuart Tower, Sulte is-bos 18bos 186,269A  33 5270-14
	A W. (15.0856152 US/0856152 US/0856152 USee Jose Adhesion Modelesion Modelesi
135 135 135 139 139 121 121 123 123 123 123	cation US/085615  Oly, Mary M. er, Olivier J. ITON: Humanized Huma
444444 444444 6000004444 6000004444	-11  Seldo29  Seldo29  TT Bendig, TT Leger, O  TT Saldanha  TT Jones, S  TT Leger, O  TT Saldanha  TT Jones, S  TH JONES, S  TATON NUMBER P  TH JONES, S  TH S
44444 44 44 44 44 44 44 44 44 44 44 44	RESULT 1  US-08-561-521-11  Sequence 11, Application US/08561521 Patent No. 5840299 GENERAL INFORMATION: APPLICANT: Bendig, Mary M. APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier J. APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier J. APPLICANT: Leger, Olivier J. APPLICANT: Saldanha, Jose APPLICANT: Jones, S. APPLICANT: Jones, S. TITLE OF INVENTION: Humanized Antil TITLE OF INVENTION: Adhesion Molecu NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsend STRET: One Market Plaza, Steuar CITY: San Francisco STRET: California COUNTRY: USA ZIP: 94105 COMPUTER READALE FORM: MEDIUM TYPE: Floppy disk COMPUTER: BM PC Compatible ODERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIN Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/561,52; FILING DATE: CLASSIFICATION NUMBER: US/08/561,52; FILING DATE: 25-JAN-1994 ATTORNEY/AGENT INFORMATION: NAME: SMILL, William L. REGISTRATION NUMBER: 15270-1 TELEPHONE: 415-543-5043 INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 123 amino acids TYPE: amino acids STRANDEDNESS: single STRANDEDNESS: single STRANDEDNESS: single STRANDEDNESS: single
00012m45000000000000000000000000000000000000	RESULT 1 US.08-561   Sequence   Patent     APPL   APPL     APPL   APPL     TITL   TITL     TIT

121 VSS 123

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                                                                           DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY
                                                                                                                                                                                                                                                                                    Sequence 11, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Loger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 25-JAN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNAGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15270-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
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Best Local Similarity 100.0
Matches 123; Conservative
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MOLECULE TYPE: protein
PCT-US95-01219-11
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
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PCT-US95-01219-11
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61 DPKFQGRVT1TADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 655; DB 2; Length 142; 100.0%; Pred. No. 1.6e-58; Live 0; Mismatches 0; Indels (
                                                            GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORREY/AGENT INFORMATION:
NAME: Smith, William L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15270-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
PCT-US95-01219-17
Sequence 17, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-561-521-17; Sequence 17, Application US/08561521; Patent No. 5840299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Smith, William L. REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 15 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                               94105
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               APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
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Patent No. 5840299
Patent No. 5840299
Patent No. 5840299
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saidanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: 445
NUMBER OF SEQUENCES: 45
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ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECHONE: 415-543-9600
TELEFAX: 415-543-9603
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Saldanha, Jose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0
Best Local Similarity 100.0
Matches 123; Conservative
                                                                                                                                                   STREET: ONE MALLES
CITY: San Francisco
cmaTE: California
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61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF ENVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 123;
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                                 COMPUTER SALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEN PC Compatible
COMPUTER: TEN PC Compatible
COMPUTER: TEN PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE: US/08/561,521
FILING DATE: US/08/186,269A
PRIOR APPLICATION: A24
PRIOR APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 15270-14
TELEPHONE: 415-543-5600
TELEPHONE: 415-543-5043
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTER STICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Dar PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
ADPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
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84.3%; Score 552; DB 2;
Best Local Similarity 82.9%; Pred. No. 2.8e-48;
Matches 102; Conservative 11; Mismatches 10.
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-9
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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PCT-US95-01219-9
COUNTRY:
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PCT-US95-01219-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
ATTILE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                    84.3%; Score 552; DB 5; Length 123;
82.9%; Pred. No. 2.8e-48;
Live 11; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William 10,23
REGIERATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 15270-14
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                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 82.9%
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  San Francisco
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-561-521-4
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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61 DPKFQGRVTITADISASTAYMELSSLRSEDIAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                     20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                     1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                          Length 140;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     Ouery Match
83.1%; Score 544; DB 2;
Best Local Similarity 82.6%; Pred. No. 2.1e-47;
Matches 100; Conservative 11; Mismatches 10
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FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Smith, William L. REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15;
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                            SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
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amino acid
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                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-4
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                                                                                                                                                                                                                        Query Match
Best Local Similarity
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83.1%; Score 544; DB 5; Length 140;

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61 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 114
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 117;
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                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: OHTOMO, TOSHIHIKO
APPLICANT: SATO, KOH
APPLICANT: TSUCHIYA, MASABUKİ
TITLE OF INVENTION: RESHARABD HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDÜLLÜBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 523; DB 4;
Pred. No. 2.1e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US/08/646,265A
09-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53466/184
                                                                                                                                                                                              Sequence 132, Application US/08646265A Patent No. 6214973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELERA: 904136
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEGNER, Harold C.
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83.78;
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                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & La
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 09 CLASSIFICATION:
                                                                                                                                                       RESULT 10
US-08-646-265A-132
                                                                                 118 VSS 120
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NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS: CARRESPONDENCE ADDRESS: SEED and BERRY SITREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                           61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                             20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCHVKQRPEQGLEWIGRIDPANGYTKY 79
                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Pred. No. 2e-45;
8; Mismatches 10; Indels 3
                10; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; Pred. No. 2.1e-47;
11; Mismatches 10
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/871,488A
FILING DATE: 09-JUN-1997
                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/08871488A Patent No. 6358710 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sharkey Ph.D., Richard G. REGISTRATION NUMBER: 32,629
                                                                                                                                                                                                                                                                                                                                                                                                                               Reno, John M.
Mallett, Robert W.
Hylarides, Mark D.
Searle, Stephen M.J.
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82.9%;
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82.6%;
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Pedersen, Jan T.
Rees, Anthony R.
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                  Matches 100; Conservative
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STATE: Washington
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                   RESULT 9
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53466/184
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TELECOMMUNICATION:
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INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
                                                                                                                                                                           COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : MOLECULE TYPE: protein US-08-646-265A-109
                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWYRQAPGQGLEWMGRIDPADGNTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.8%; Score 523; DB 4; Length 136; 83.7%; Pred. No. 2.5e-45; tive 4; Mismatches 10; Indels
                                                                 GENERAL INCORMATION:

GENERAL INCORMATION:

APPLICANT: SATO, KOh

APPLICANT: TSUCHIYA, MASSAYUKI

TITLE OF INVENTION: RESHARED HUMAN ANTIBODY TO HUMAN

TITLE OF INVENTION: MEDULLOBLASTOMA CELLS

NUMBER OF SEQUENCES: 132

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/646,265A FILING DATE: 09-SEP-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFRAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 109, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, TOShihiko
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
              US-'08-646-265A-99; Sequence 99, Application US/08646265A; Patent No. 6214973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELER: (202,...
TELER: 904136
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
"VDR: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 83.7
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                     CITY: Washington
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US-08-646-265A-109
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                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                        STATE:
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RESULT 11
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61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Best Local Similarity 83.7%; Pred. No. 5.7e-45;
Matches 103; Conservative 4; Mismatches 10; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Andanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
APPLICANT: SATO, KOH
APPLICANT: TSUCHIYA, MASAYUKI
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR ADPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HAROLD C.
                                                                                                          STREET: 8000 K Street, N.W., Suite 500 CIT: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.6%; Score 515; DB 2; Length 119; 82.9%; Pred. No. 1.4e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Indels
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/08/186,269A
FILING DATE: 25-JAN-1994
ATORNEY/AGENT INFORMATION:
NAME: Smith, William L.
NAME: Smith, William L.
RECISTRATION NUMBER: 30,223
RECISTRATION NUMBER: 15270-14
TELEPHONE: 415-543-9600
TELEFAX: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 102; Conservative
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STATE: California
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                                                                    STATE: CA
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61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldania.
APPLICANT: Saldania.
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
CORRESPONDENCE: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 78.6%; Score 515; DB 5; Length 119; Best Local Similarity 82.9%; Pred. No. 1.4e-44; Matches 102; Conservative 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
     PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                     UMBER: PCT/US95/01219
25-JAN-1995
                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTONEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPBRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08561521 Patent No. 5840299 GENERAL INFORMATION:
                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 15.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-5043
TELERAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGIH: 119 amino acids
SOFTWARE: Patentin Rel.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                             CLASSIFICATION:
                                                                        FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
78.2%; Score 512; DB 2; Length 119;
Best Local Similarity 82.9%; Pred. No. 2.7e-44;
Matches 102; Conservative 4; Mismatches 13; Indels
NAME: Smith, William L.

REGISTRATION NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEPHONE: 415-643-9600
TELEPHONE: 415-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: January 6, 2003, 13:19:10
Job time: 11.1879 secs
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REFERENCE/DOCKET NUMBER: 46
TELECOMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
TELEFAX: 973-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 117 AMINO ACIDS TYPE: AMINO ACID
442
439
437.5
436.5
436.5
                                                                                                                    Sequence 53, Appl
Sequence 77, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 1, Appl
Sequence 6, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 19, Appli
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Sequence 1, Appli
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Sequence 2, Appli
Sequence 6, Appli
                                                                                   January 6, 2003, 13:17:36; Search time 5.96364 Seconds (without alignments) 390.875 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16,
                                                                                                                                                                     1 QVQLVQSGAEVKKPGASVKV......NYGVYAMDYWGQGTLVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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/cgn2_6/ptodata/2/pubpaa/USOB_USUBCOMB.pep:*
         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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2 US-10-025-687-2

3 US-09-48-960-6

0 US-09-753-436-86

0 US-09-753-436-86

0 US-09-956-206A-77

0 US-09-917-1

0 US-09-917-410-6

0 US-09-917-410-6

0 US-09-917-48

0 US-09-917-48

0 US-09-917-48

0 US-09-917-9-8-8

0 US-09-917-9-8-9

0 US-09-918-9-55-9

10 US-09-919-55-11

10 US-09-911-737-16

10 US-09-911-737-16
                                                                                                                                                                                                                                                                Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                      117078 seqs, 18951520 residues
                                                                                                                                                                                                                                                                                                                                                                                        Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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448.5
4447.5
4447.5
4467.5
446.5
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472
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469
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451.5
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Maximum DB
                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                      Run on:
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Sequence 2, Appli
Sequence 17, Appli
Sequence 17, Appl
Sequence 27, Appl
Sequence 78, Appl
Sequence 63, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 76, Appl
Sequence 76, Appl
Sequence 76, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
TITLE OF INVENTION: Respiratory Syncytical Virus
COMPRES OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, ADDRESSEE: STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD STREET: 6 BECKER FARM ROAD STATE: NEW JERSEY
                                  US-10-047-542-47

US-09-976-118-2

US-09-811-737-9

US-09-811-737-17

US-09-811-737-17

US-09-911-737-17

US-09-956-206A-63

US-09-956-206A-63

US-09-956-206A-63

US-09-956-206A-63

US-09-956-206A-63

US-09-956-206A-63

US-09-825-012-86

US-09-825-012-86

US-09-825-012-90

US-09-825-012-50

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US-09-825-012-50
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COMPUTER: P160
SOFTWARE: MS Word 97
SOFTWARE: MS Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,120A
FILING DATE: September 21, 1998
CLASSIFICATION: September 21, 1998
CLASSIFICATION: DATA:
APPLICATION NUMBER: 08/290,592
FILING DATE: Angust 15, 1994
APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991
ATTORNEY, AGENT INFORMATION:
NAME: Olstein Filing ATTORNEY, ADDITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09158120A
Patent No. US20020102257A1
GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 070bb
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
^AMDITTER: P160
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469201-367

Mon Jan

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TYPE: PRT
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TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; |OTHER INFORMATION: Human consensus antibody heavy chain variable region US-10-025-687-2
                                                                                                                                                                                                                                                               61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AQKFQGRVIMTRDKSSSTAYMELSSLRSEDTAVYYCAR---WGGDGFYAMDYWGQGILVT 117
                                                                                                                                 Gaps
                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYXIXWVRQAPGQGLEWIGWIDPENGNIVF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Gaps
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                                                                                   Query Match 75.1%; Score 492; DB 10; Length 117; Best Local Similarity 78.0%; Pred. No. 2.5e-33; Matches 96; Conservative 7; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brettman, Lee R.
APPLICANT: Fox, Judith A.
APPLICANT: Allison, David Edward
APPLICANT: Allison, David Edward
TITLE OF INVENTION: Method of Administering an Antibody
FILE REFERENCE: 1855.2007-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/025,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/748,960
CURRENT FILING DATE: 2000-12-27
CRED DATE: 2000-12-27
PRIOR APPLICATION NUMBER: US 09/550,082
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEG ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10025687
Patent No. US20020142255Al
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                    MOLECULE TYPE: PROTEIN
TOPOLOGY: LINEAR
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                                         US-09-158-120A-17
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US-10-025-687-2
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                                                                                   Query Match
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61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                 20 QVQLVQSGAEVKKPGASVKVSCKGSGYTFTSYMMHWVRQAPGQRLEWIGEIDPSESNTNY 79
                                                                                                                   FEATURE:
OTHER INFORMATION: Portion of the heavy chain of LDP-02 with a heavy
OTHER INFORMATION: chain signal peptide
                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                      73.9%; Score 484; DB 10; Length 180; 76.4%; Pred. No. 1.6e-32; tive 9; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-09-753-436-53
Sequence 53, Application US/09753436
Sequence 53, Application US/09753436
Patent No. US20010029293A1
GENERAL INFORMATION:
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 APPLICATION DATA:
APPLICATION NUMBER: US/09/753,436
FILING DATE:
                                                                                                                                                                                     NAME/KEY: SITE

LOCATION: (19)...(20)

OTHER INFORMATION: signal peptide cleavage site
US-09-748-960-6
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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APPLICATION NUMBER: US 08/487,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 08/286,754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
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COMPUTER READABLE FORM:
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                                             LENGTH: 180
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                      SEQ ID NO 6
                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 86, Application US/09753436
Patent No. US20010029293A1
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: VAZEUX, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Mismatches
                  FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION APPLICATION DATA:
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US 07/889,724
                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/382,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995
                                                                                                                                                                                                                                                                                                                             : 123 amino acids
amino acid
                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 72.2%
Best Local Similarity 78.0%
Matches 96; Conservative
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APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 6300 Sea
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
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APPLICANT: DO COUTO, FERNANDO J.R.
CERIANI, ROBERTO L.
PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
MG3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
MG7 HUMANIZING ANTIBODY PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 QVQLVQSGAEVKKPGASVKVSCKASGYIFTVYWWHWVRQAPGQGLEWMGYINPNTDYTEY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.1%; Score 472; DB 10; Length 123; Best Local Similarity 77.2%; Pred. No. 1e-31; Matches 95; Conservative 8; Mismatches 16; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/956,206A FILING DATE: 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                             PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-UNN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY AGENT INFORWATION:
                                      UMBER: US 08/009,266
22-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 77, Application US/09956206A Patent No. US20020164339Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  NAME: Williams, Joseph A., Jr. REGISTRATION VUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 86:
FILING DATE: 05-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 123 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-09-753-436-86
               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                           FILING DATE:
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Sequence 28, Application US/09859053
Patent No. US20020102658A1
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: TSU11, Takashi
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658A1uaki
APPLICANT: Hori, No. US20020102658A1uaki
APPLICANT: HORI, No. OSSIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 YDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGN----YGVYAMDYWG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.6%; Score 469; DB 9; Length 129; 76.0%; Pred. No. 1.9e-31; Live 3; Mismatches 22; Indels
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                                                                                                                                                                                                                                                            NAME: WITT, ERIC
REGISTRATION NUMBER: 44,408
REFERENCE/DOCKET NUMBER: 276332000101
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 813-560
TELEFAX: (650) 494-0792
TELEFAX: 70611
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/525,539
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/US95/11683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR PELLING DATE: 2001-09508
PRIOR FILING DATE: 2001-03-30
PRIOR PELLING DATE: 2000-05-18
PRIOR PELLING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 77:
                                                                                                             PILING DATE: 14-5ER-1995
APPLICATION NUMBER: 08/487,598
FILING DATE: 7-JUNE-1995
APPLICATION NUMBER: 08/307,868
FILING DATE: 16-SEPT-1994
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 129 amino acids
                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
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93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 QGTLVTVSS 123
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Gaps

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Best Local

Matches

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TITLE OF INVENTION STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/025,687
CURRENT FILING DATE: 2002-04-17
WUMBER OF SEC ID NOS: 28
SOFTWARE: Patentin version 3:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR PREVENTION OF ACUTE ORGAN DAMAGE AFTER EXTRACORPOREAL BLOOD CIRCULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Human consensus antibody heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
                                                                                                                  80 AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARTYYYDSSGYYHDAFDIWGQGTM 139
                                                                                            61 DPKFQGRVTITADISASTAYMELSSLRSEDTAVYYCAREGYYGNYGVY -- AMDYWGQGTL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AQKFQGRVIITADESTSTAYMELSSLRSEDTAVYYCAR---WGGDGFYAMDYWGQGTLVT 117
                        20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEMMGWINPHSGGTNY 79
1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYŢKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.2%; Score 459.5; DB 12; Length 120; Best Local Similarity 77.2%; Pred. No. 1e-30; Matches 95; Conservative 2; Mismatches 23; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09917410 Patent No. US20020098183A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10025687 Patent No. US20020142255A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York COUNTRY: U.S.A. ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                     119 VTVSS 123
                                                                                                                                                                                                                                     140 VTVSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 VSS 123
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LENGTH: 120
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US-09-917-410-6
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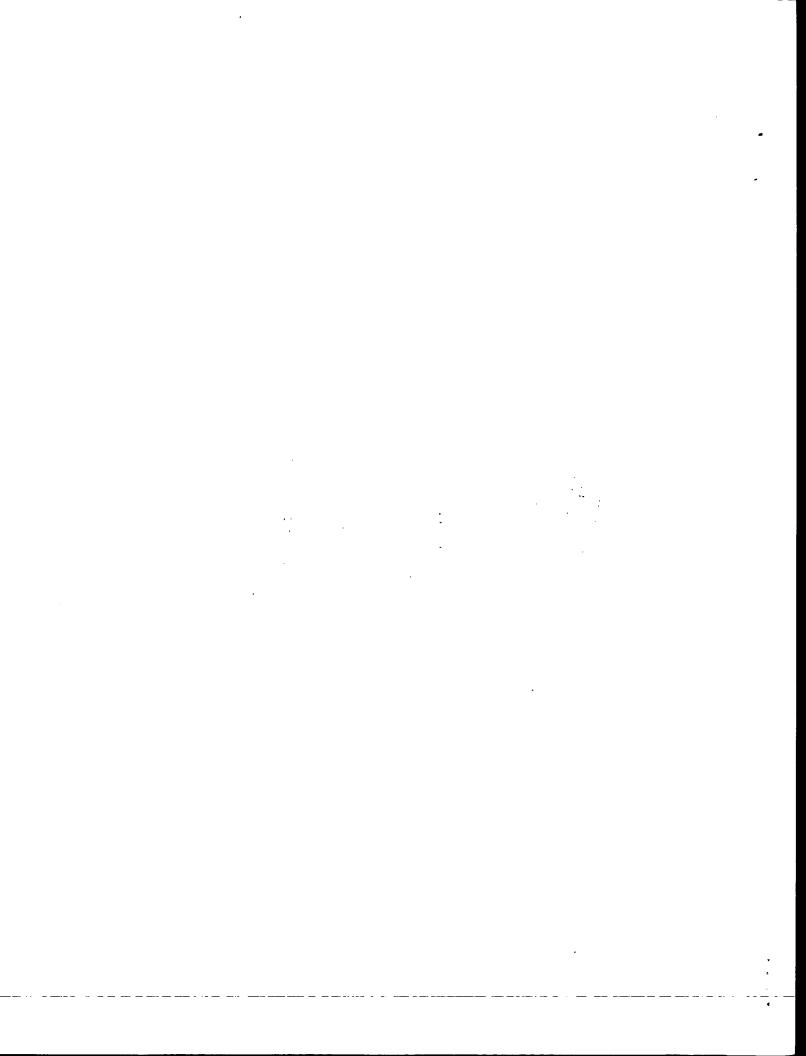
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FILING DATE: 06/20/96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 TLVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TLVTVSS 127
                                                                                                                                                                                                                                                                                                              US-08-779-457-48
                                                                                                                                                                                                                                                                           TYPE: Am. TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-09-760-723-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 139
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                                                                                                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
69.8%; Score 457; DB 10; Length 448;
Best Local Similarity 75.6%; Pred. No. 5.8e-30;
Matches 93; Conservative 8; Mismatches 20; Indels
                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kyung, Jin Kim
APPLICANT: Matthews, Milliam
APPLICANT: Redrigues, Maria L.
TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
COMRESPONDENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   NAME: Hanson, No. US20020098183Alman D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: 3.5 inch, 1.44 Mb floppy disk IBM PC compatible
                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: CURNOWN>
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/917,410
FILING DATE: 26-Jul-2001
CLASSIFICATION: <unknown>
                   SOFTWARE: ASCII, WordPerfect 5.1
 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 448 amino acid residues TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                        ; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-917-410-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/779,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 48, Application US/08779457 Publication No. US20020193571A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/667197
                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Chiang, Nancy Y.
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
SOFTWARE: WinPat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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US-08-779-457-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCA----REGYYGNYGVIAMDYWGQG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 SQKFKGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGLRRGGYY------FDYWGQG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYG----NYGVYAMDYWGQG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AQKFQCRVTWTRDTSIGTAYMELSKLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Gaps
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Live 6; Mismatches 18; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.6%; Score 456; DB 1; Length 249; 70.9%; Pred. No. 4e-30; Live 11; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVESTION INHIBITOR OF LYMPHOCYTE ACTIVATION
TITLE OF INVESTION INHIBITOR OF LYMPHOCYTE ACTIVATION
FILE REFERENCE: 053466/0295
CURRENT APPLICATION NUMBER: US/09/760,723
CURRENT FILING DATE: 2001-05-29
FRIOR APPLICATION NUMBER: 09/367,833
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PALENTIN Ver. 2.1
                                                                                                                                                                     REFERENCE/DOCKET NUMBER: P0986P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09760723 Patent No. US20020034507Al GENERAL INFORMATION:
                                08/585005
                                                                                                                  NAME: Lee, Wendy M. REGISTRATION NUMBER: 40,378
                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                          TELEPHONE: 415/225-1994
TELEFAX: 415/952-981
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/56
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       : 249 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 69.6%
Best Local Similarity 70.9%
Matches 90; Conservative
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Matches 92; Conservative
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SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 QVQLVQSGAEVKKPGASVKVSCKASGYTFTPYWMQWVRQAPGQGLEWMGSIFPGDGDTRY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence H chain V region version s of OTHER INFORMATION: anti-HMI.24 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 139;
                                                                                                                                                                                                                                       APPLICANT: KOISHIRARA, YASUO
APPLICANT: YOSHINURA, YASUO
APPLICANT: YOSHINURA, YASUO
APPLICANT: YOSHINURA, YASUOI
TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
FILE REPERENCE: 053466/0255
CURRENT APPLICATION NUMBER: US/09/355,925
CURRENT APPLICATION NUMBER: PCT/JD98/00568
PRIOR APPLICATION NUMBER: PCT/JD98/00568
PRIOR FILING DATE: 1998-02-12
PRIOR PILING LATE: 1997-02-12
PRIOR FILING DATE: 1997-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oulery Match 68.9%; Score 451.5; DB 10; Length Best Local Similarity 72.4%; Pred. No. 5.2e-30; Matches 92; Conservative 6; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KOLSHIHARA, YASUO
TITLE OF INVENTION: INHIBITOR OF LYMPHOCYTE ACTIVATION
TITLE OF INVENTION: INHIBITOR OF LYMPHOCYTE ACTIVATION
FILE REFERENCE: 053466/0295
CURRENT APPLICATION NUMBER: US/09/760,723
CURRENT FILING DATE: 10908-08-29
PRIOR APPLICATION NUMBER: PCT/JF98/00831
PRIOR PELLING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 8
SOTTWARE: PATENTIN VET. 2.1
                                                                                                                                                                     ; Sequence 8, Application US/09355925
; Patent No. US20020037288A1
; GENERAL INFORMATION:
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Patent No. US20020034507A1
GENERAL INFORMATION:
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                                             133 TTVTVSS 139
117 TLVTVSS 123
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                                                                                                                     RESULT 12
US-09-355-925-8
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LENGTH: 139
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                                                                                                                                           18; Indels 11; Gaps
                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Amino acid; CTHER INFORMATION: sequence of H chain V region version r of; OTHER INFORMATION: humanized anti-HMI.24 antibody US-09-355-925-7
                                                                                 Score 448.5; DB 10; Length 139;
Pred. No. 9e-30;
7; Mismatches 18; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 68.5%; Score 448.5; DB 10; Length 139; Best Local Similarity 71.7%; Pred. No. 9e-30; Matches 91; Conservative 7; Mismatches 18; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KOISHIHARA, YASUO
APPLICANT: KOISHIHARA, YASUO
APPLICANT: YOSHIMURA, YASUSHI
TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
FILE REFERENCE: 053466/0255
CURRENT APPLICATION NUMBER: 105/09/355,925
CURRENT FILING DATE: 1999-08-11
CURRENT FILING DATE: 1999-08-11
OTHER INFORMATION: anti-HM1.24 antibody
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JMBER: JP 9-41410
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APPLICANT: Athwal, Dilject Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/09949559 Patent No. US20020151682A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 7, Application US/09355925 ; Patent No. US20020037288A1
                                                                                    68.5%;
71.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/
PRIOR FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: JP 9
PRIOR FILING DATE: 1997-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                        Ouery Match 68.5%
Best Local Similarity 71.7%
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                     117 TLVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 TTVTVSS 139
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                       US-09-760-723-7
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5.1.3
Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2003
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OM protein - protein search, using sw model

January Run on:

6, 2003, 13:12:26 ; Search time 11.4303 Seconds
 (without alignments)
 1034.490 Million cell updates/sec

1 QVQLVQSGAEVKKPGASVKV......NYGVYAMDYWGQGTLVTVSS 123 US-09-155-739-11 655 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\* Database :

pirl:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		ф			CHINATIO	
Result No.	Score	Query Match	Length	DB	ID	Description
	488.5	74.6	178	-	229594	To camma chain (WM
2			120	10	34	g beave chain V
m	473.5	72.3	118	2	526	chain V
4	9	ij	123	7	D33548	d heavy
5	467	ä	142	7	248	q heavy chain V
9		ä	117	~	S17586	g heavy
7	459.5	ö	122	~	806823	g heavy
æ	56.	6	132	7	PH0954	q heavy
6	455	6	116	~	S24289	ים
10	455	6	221	7	S49220	-
11	450	8	129	7	S46393	6
12	449	8	115	7	S03482	g heavy
13	447.5	8	135	~	849530	'n,
14	4	ж.	120	~	503484	heavy
15	446.5	ъ.	136	7	РН0960	
16	444	۲.	136	7	S04576	
17	マ	7	119	7	PH0961	heavy chain
18	441.5	67.4	268	~	A56446	Iq heavy chain V r
19	439.5	7	104	7	PH1665	heavy
20	9	67.1	114	4	A47271	trophen
21	3	۲.	133	7	354	g heavy cha
22	m	ζ.	627	~	S14683	Ig mu chain precur
23	ω.	9	114	~	PH1667	g heavy cha
24	38.	9	118	~		ь
25	7	ė.	137	~	_	Iq heavy chain V r
26	36.		120	7	S31999	Ig heavy chain V r
27	35.	ė.	120	~	10	Ig heavy chain V r
28	35.	ė.	128	7	10	Ig heavy chain V r
29	ë.	9	126	7		Ig heavy chain V-1

										y chain V r				vy chain V r	v chain V r
Ig heav	Ig heav	Ig heav	Ig heav	Ig heav	Ig heav	Ig heav	Ig heav	Iq heav	Ig heav	Ig heavy	Ig heav	Ig gamm	Iq qamm	Iq heavy	Ig heav
PH0955	PH0953	144151	PH1012	PH0957	ElHUND	868170	A33548	S34014	S36260	PH1561	S23623	838950	S40295	PH1426	520783
7	7	7	2 E	7	-	~	7	7	2	147 2 PH1561	7	7	7	7	7
127 2 F	135 2 F	126 2 1	108 2 F	125 2 F	143 1 F	125 2 8	129 2 #	127 2 8	129 2 8	7	171 2 9	246 2 8	446 2 5	122 2 1	121 2 9
66.1 127 2 F	66.1 135 2 F	65.8 126 2 1	65.6 108 2 F	65.5 125 2 F	65.3 143 1 E	65.2 125 2 8	65.2 129 2 #	65.0 127 2 8	64.9 129 2 8	147 2 F	64.8 171 2 5	64.3 246 2 8	64.3 446 2 5	64.2 122 2 E	64.1 121 2 9

# ALIGNMENTS

61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120 ŏ

74 DPKFQGKATITADTSTNTAYLQLSSLTSEDTAVYYCTG----GNY-AYGMDYWGQGTSVT 128 qq

|||| VSS 131 121 VSS 123 129 δý g

RESULT 2
S03471
19 heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Sap-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000
C.Accession: S03471; S07453
R.Roca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four antihypervariable regions.
A;Reference number: S03471; MUID:84057768; PMID:6416834

A Molecule type: mRNA Sesion: \$03471
A Molecule type: mRNA Sesidues; 7-120 CROCI>
A CROSS-references: EMBL:X01820; NID:951833; PIDN:CAA25962.1; PID:91333983
A) Note: this sequence was determined from the differentiated gene R:Rocca-Serra, J; Mazie, JC; Moinier, D; Leclercq, L.; Somme, G.; Theze, J.; Foug J. Immunol. 129, 2554-2558, 1982
A) Immunol. 129, 2554-2558, 1982
A) Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not

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A;Molecule type: mRNA
A;Residues: 1-123 <KIP>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A; Accession: S17586
                                                                                                                                                                                          Query Match
Best Local Similarity 74.8%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CiSpecies: Homo sapiens (man)
CiDate: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
CiAccession: S36265
RiGitfiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.Embo J. 12, 725-734, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: $36256; MUID:93178448; PMID:7679990 A;Accession: $35265 A;Accession: $35265 A;Status: preliminary; nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGOGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYXCARDFLSGY------LDYWGQGT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-118 <GRI>A; Cross-references: EMBL:218846; NID:933121; PIDN:CAA79298.1; PID:9339900 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQCLEWMGWINPNSGGTNY 60
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                                                                                                                                                                                                                                                                                       Length 120;
                          A;Accession: S07453
A;Molccule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamilly: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                      15; Indels
A; Reference number: S07453; MUID:83058021; PMID:6815271
                                                                                                                                                                                                                                                                            Score 477; DB 2;
Pred. No. 8.8e-36;
                                                                                                                                                                                                                                                                                                                                                  11; Mismatches
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                                                                                                                                                                                                                                                                               72.8%;
75.6%;
                                                                                                                                                                                                                                                                                                                                                      93; Conservative
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S17586
S17586
Ig heavy chain V region (E8) - mouse (fragment)
Ig heavy chain V region (E8) - mouse (fragment)
Ig heavy chain V region (E8) - mouse)
Ig heavy chain Wisconsing (house mouse)
C; Speciess in musculus (house mouse)
C; Paccession: S17586
E; Paterson, Y; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A; Title: Blochemical implications from the variable gene sequences of an anti-cytochr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 12-0ct-1889 #sequence_revision 12-0ct-1889 #text_change 16-Aug-1996
C;Accession: A32483
R;Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck
Blochem. Blophys. Res. Commun. 160, 1250-1256, 1989
A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells
A;Reference number: A32483; MUID:89273586; PMID:2499327
A;Residues: 1-142 < LAR>
A;Residues: 1-142 < LAR>
A;Gross-references: GB:M26463
C;Superfamily: immunoglobulin V region: immunoglobulin homology
C;Superfamily: immunoglobulin homology
C;Superfamily: immunoglobulin homology
C;Superfamily: immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                               61 AEKFQGRVTITRDTSINTAYMELSRLRSDDTAVYYCARASYCGYDCYYFFDYWGQGTLVT 120
                                                                                  Gaps
                                                                                                                                                                                                                                                                                        61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAREKLATTIFGVLIITGMDYWGQG 130
                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                     Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.3%; Score 467; DB 2; Length 14.273.2%; Pred. No. 8.2e-35; Mismatches 22; Indels
71.5%: Score 400,
74.8%; Pred. No. 5.7e-35;
.tive 7; Mismatches 24; Indels
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C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM
F:31-35/Region: complementarity-determining
F:36-50/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 VWGQGTTVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                112 YWGQGTLVTVSS 123
                                                                                                                                                                                           Query Match
Best Local Similarity
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A:Molecule type: mRNA
A;Residues: 1-116 <MON>
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S24289
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J. Mol. Biol. 209, 763-778, 1989
Aritle: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A: Reference number: S06815; MUID:90064531; PMID:2555519
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C;Sacession: PH0913 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0954
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Fille: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region (clone IIc) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S06823
                                                                                                                                                                                                                                                                                                61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY-YGNYGVYAMDYWGQGTLV 119
                                                                                                                                                                                                                                                                                                                        60 YDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLV 119
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                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIH-WVRQAPGQRLEWMGRIDPANGYTK 59
                        A;Cross.references: EMBL:X60683; NID:951820; PIDN:CAA43095.1; PID:951821
C;Superfaaily: immuuoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                              Length 117;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-99/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: Î-132 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                     11; Indels
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                                                                                                                              DB 2;
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                                                                                                                                                    Pred. No. 1e-34;
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                                                                                                                                                                        15; Mismatches
                                                                                                                              71.0%; Score 465; 72.6%; Pred. No. 1
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                                                                                                                                             Best Local Similarity 72.6%
Matches 90; Conservative
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Matches 91; Conservative
    A; Residues: 1-117 <MYL>
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Gramma-1 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C;Accession: S49220
R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
Submitted to the EMBL Data Library, September 1994
A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing A;Reference number: S49220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, September 1991
A; Description: Cloning and sequencing of the cDNA coding for the variable regions of
A; Reference number: S24287
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                                                                                                                                                                                                                                                                                                                                                                      61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYCARPHASIDDFWSGYYPNYYYYGMD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL:X62705; NID:g51690; PIDN:CAA44584.1; PID:g1333963 C.Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: immunoglobulin F;14-97/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 PKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-EGYYGNYGVYAMDYWGOGTLVT 120
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                                                                                                                                                                                                                           1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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6
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                                                                                                                   Length 132;
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                                                                                                                                                                          Indels
                                                                                                                   DB 2;
                                                                                                                                                                       27;
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Pred. No. 7.8e-34;
                                                                                                             Score 456.5; DB 2
Pred. No. 6.6e-34;
1; Mismatches 27
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F;51-67/Region: complementarity-determining 2 F;68-98/Region: framework 3 F;99-120/Region: complementarity-determining 3
                                                                                                                69.78;
72.08;
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71.5%;
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                                                                                                                                                                    95; Conservative
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A; Note: this sequence was determined from the differentiated gene R; Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug J. Immunol. 129, 2554-2558, 1982
A; Tille: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not A; Reference number: S07453; MUID:83058021; PMID:6815271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C:Accession: $49530
R:Wahmoudi, M.; EdWards, J.; Cairns, E.; Bell, D.
Submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: $48797
A;Rocession: $49530
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <AMA+>
A;Residues: 1-135 <AMA+>
A;Cross-references: EMBL:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-43 < ROC2>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology < IMM>
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hypervariable regions.
A;Reference number: S03471; MUID:84057768; PMID:6416834
A;Accession: S03482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.5%; Score 449; DB 2; 70.2%; Pred. No. 2.7e-33;
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                                                                                                 A; Molecule type: mRNA
A; Residues: 10-115 <ROC1>
A; Cross-references: EMBL:X03219
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Matches 85; Conservative
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Best Local Similarity
                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                              A; Accession: S07453
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S03484
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A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rifigini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.

7. Mol. Blol. 239, 68-78, 1994

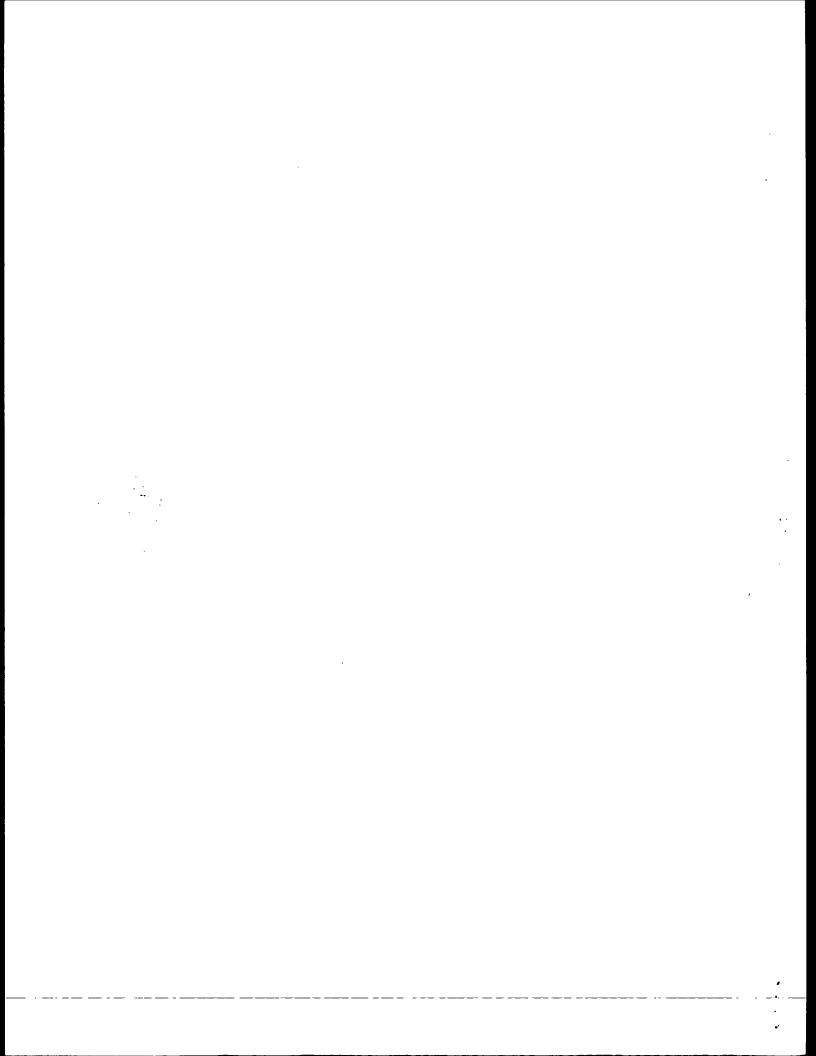
A.Title: In vitro assembly of repertoires of antibody chains on the surface of phage by A.Reference number: $46390; MUID:94254092; PMID:8196048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:231680; NID:9509786; PIDN:CAA83485.1; PID:91335146 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F:15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)
C; Species: Mus musculus (house mouse)
A; Variaty: strain BALB/C
C; Date: 26 Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C; Accession: S03482; S07453
                                           A;Cross-references: EMBL:Z37502; NID:g541778; PIDN:CAA85732.1; PID:g541779 A;Experimental source: strain Balb/c C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AQKFQGWVTMIRDISISTAYMELSRLRSDDTAVYYCARDSAYYYDSSGYXSANYYMDWG 120
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Pred. No. 1.5e-33;
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                                                                                                                                               F:111-221/Domain: V region #status predicted <VRG>F:121-221/Domain: C region #status predicted <CRG>F:139-203/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                  69.5%; Sco... 70.78; Pred. No. ...
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                                                                                                                         Keywords: immunoglobulin
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A; Residues: 1-129 <FIG>
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A; Molecule type: mRNA
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S46393
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Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment) C; Species: Mus musculus (house mouse)	C. Accession. 2014.04. 60745.2	Rivoca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M. RWAG, J. 967-873 1003	ATTLE 5. 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,	A:Reference number: S03471; MUID:84057768; PMID:6416834 A:Accession: S034844 A:Accession: S034844	i	K; MCCGA'SETIA, 0.1; MAZLA, 0.4.; MOINIBET, D.; LECLETCQ, L.; SOMME, G.; Theze, J.; Fougered J. Immunol. 129, 2554-2558, 1982 A; Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not set A; Reference number: S07453; MUID:83058021; PMID:6815271 A; Accession: S07453	A; Status: preliminary A; Molecule type: protein A; Molecule type: protein A; Mosidues: 1-43 *ROC2> C; Superfamily: immunoglobulin V region; immunoglobulin homology F; 15-98/Domain: immunoglobulin homology <imm></imm>	Query Match 68.2%; Score 447; DB 2; Length 120; Best Local Similarity 71.5%; Pred. No. 4.2e-33; Matches 88; Conservative 11; Mismatches 20; Indels 4; Gaps 1;	QY 1 QVQLVQSGAEVKRPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60 :	QY 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYCAREGYYGNYGWYAMDYWGQGTLVT 120	Qy 121 VSS 123 Db 117 VSS 119	RESULT 15	In heavy chain V region (G6+ T-L30) - human (fragment) C;Species: Homo sapiens (man) C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996	C:Accession: PHU900 Wartin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J. T. Exp. Med. 175, 983-991, 1992	A.Title: Evidence for somatic selection of natural autoantibodies. A; Meference number: PH0952; MUID:92202880; PMID:1552291 A; Accession: PH0960	A;Status: nucleic acid sequence not shown A;Molecule type: DNA B:Postfains: 1-134 Amb.	C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keyvords: heterotetramer; immunoglobulin F:1-30 Poorion: framedount 1	F:15-98/Domain: immunoglobulin homology <imm> F:15-98/Domain: immunoglobulin homology <imm> F:31-35/Region: complementarity-determining 1 F:36-50/Region: framework 2</imm></imm>	F;51-67/Region: complementarity-determining 2 F:68-98/Region: framework 3 F;99-124/Region: complementarity-determining 3	Query Match 68.2%; Score 446.5; DB 2; Length 136; Best Local Similarity 69.1%; Pred. No. 5.3e-33; Matches 94; Conservative 1; Mismatches 28; Indels 13; Gaps 1;

1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

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eau, M.	Db	61	61 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGRTRVSVSTLYDSSGYYDFSGY 120	120
anti-GAT	Qy	108	108 YAMDYWGQGTLVTVSS 123	
	q a	, 121		
	Sea	arch com time	Search completed: January 6, 2003, 13:18:20 Job time : 12.4303 secs	



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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 6, 2003, 12:48:25; Search time 6.21212 Seconds (without alignments) 821.231 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-155-739-11 655 1 QVQLVQSGAEVKKPGASVKV......NYGVYAMDYWGQGTLVTVSS 123

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Score 427.5			DB	SUMMARIES  ID  HVIC_HUMAN  HVIC_HUMAN	ptior home
	62.4	139		HV03_MOUSE HV07_MOUSE HV1R_HIMAN	P01747 mus musculu P01751 mus musculu P01743 homo sapien
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333	50.	117		HV10_MOUSE	
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6	50.	117	1	HV49_MOUSE	mus
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	ALIGNMENTS  PRT; 147 AA. sequence update) annotation update) UD precursor (Fragm as; Catarrhini; Hom as; Catarrhini; Hom as; Catarrhini; Hom anination of the ge in expressed in a m a. 79:6661-6665(19 a. 0., von Bahr-Lind a. 0., von Bahr-Lind a. 0., von Bahr-Lind a. 0., von Bahr-Lind a. 10., von Bahr-Lind a.	Score 427.5;   Pred. No. 3.2e ; Mismatches ; GENIKDTYIHWVR   :  :   :   SGYTFIDSYIHWIR   : :  :  :
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"The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";
Eur. J. Immunol. 12:1023-1032(1982).
- MISCELLAMBOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 AA; 13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-83131846; PubMed-6186498;
Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 409; DB 1;
Pred. No. 1.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HV07_MOUSE STANDARD; PRT; 139 AA. P01751; P01752; 21-JUL-1986 (Rel. 01, Created) 15-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) Ig heavy chain V region B1-8/186-2 precursor.
                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Mismatches
                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region 36-65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P01789, 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.48;
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                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEGMENT, JH2.
PIR; A02028; HVMSG7.
                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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                                                 116 GTLVTVSS 123
                                                                                             140 GITVIVSS 147
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                                                                                                                                                             HV03_MOUSE
P01747;
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                                                                                                                                                                                         HV03_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
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                                                                                                                                                                   RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
HV07_MO
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                                                                            "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.", cell 24:625-637(1981).
-!- MISCELLANBOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG HEAVY CHAIN V REGION B1-8/186-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.4%; Score 408.5; DB 1
62.6%; Pred. No. 2.4e-34;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A02034; MHMS18.
HSSP; PO1810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J00529; AAA38170.1; -.
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                                                                                                                                                                                                                                (NPB ANTIBODIES).
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139
139 AA;
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                                                   Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 VSS 123
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P01743;
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NON_TER
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V-I REGION HG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 405; DB 1; Length 11
Pred. No. 4.5e-34;
5; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 117
117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;
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15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.8%; Score 405; 79.6%; Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin V region; Signal.
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                                                                                                                                                                                                                                                                                                                                                     EMBL; J00240; AAA52988.1; -.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Matches 78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
(VH) gene subgroups.";
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ID HV02_MOUSE
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SEQUENCE
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RRT PRESENTATION OF THE PR
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                                                                                                                                                                                                                                                  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                      20 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWYKQRPGQGLEWIGYINPGNGYINY 79
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-88296408; PubMed-2841108; Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q., Ohno H., Fukuhara S., Honjo T., "Dispersed localization of D segments in the human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                 60.9%; Score 399; DB 1; Length 140; 61.0%; Pred. No. 2.2e-33; ive 19; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V-I REGION V35
                                                  IG HEAVY CHAIN V REGION 93G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Indels
                                                                                                                                                    27; Indels
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                                                                                 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V-I region V35 precursor.
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5; Mismatches
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HSSP; P01772; 2FB4.
INTERPRO; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Fram, PF00047; Ig; I.
SMART; SMO406; IGV; I.
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01-NOV-1991 (Rel. 20, Last seq
15-JUL-1999 (Rel. 38, Last anno
                                                                                                                                  61.0%;
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                                                                                                                                                  75; Conservative
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140
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                                                                                                                                    Sest Local Similarity
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P23083;
                                                                  NON_TER
SEQUENCE
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Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.; "A V region determinant (idiotope) expressed at high frequency in B lymphocytes is encoded by a large set of antibody structural genes."; EMBO J. 3:517-523(1984).
PIR; A02040; MHMS38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DPKFQGRVT1TADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                          rearrangements in heavy chain V-region gene segments.";
Nature 28:35-40(1980).
-!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
WHICH OCCUR IN THE D AND J SEGMENTS.
-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                            Schilling J., Clevinger B., Davie J.M., Hood L., \, "Amino acid sequence of homogeneous antibodies to dextran and DNA
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 57.7%; Score 378; DB 1; Length 117; Best Local Similarity 58.5%; Pred. No. 2.4e-31; Matches 72; Conservative 20; Mismatches 25; Indels
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NON_TER 117 117

SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
pheavy chain V region AC38 205.12.
Mus musculus (Mouse)
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J SEGMENT.
BY SIMILARITY.
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                                                                           MEDLINE=80078170; PubMed=6765983;
                                                                                                                                                                                                                                                    Interpro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART: SM00406; IGv; 1.
Immunoglobulin V region.
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InterPro: IPR003596; Ig_w.
Pfam: PF00047; ig; 1.
SMART: SM00406; IGv: I.
Immunoglobulin V region.
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HSSP; P01789; 1MCP.
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                            NCBI_TaxID=10090;
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P06330;
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DISULFID
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AQKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA----GGYGIYSPEEY-NGGLVT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRSAIIWVRQAPGQGLEWMGGIVPMFGPPNY 60
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                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V. I region EU.
Homo sapiens (Human).

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds "; Biochemistry 9:1188-1196(1970).

-I - MISCELLANBOUGS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.

PIR; AD7023; GIHUEU.

HSSP: P01772: ZFB4.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_V.

SMART; SM00406; Ig; 1.

Immunoglobulin V region.
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                            61 DPKFQGRVTITADISASTAYMELSSLRSEDIAVYYCAR 98
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
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                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gall W.E., Edelman G.M.;
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96
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Best Local Similarity
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P01757;
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SEQUENCE
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DISULFID
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-i- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
                                                                                                                                                                                                                                                  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE-83075344; Pubmed-6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (COMPLEX).
                                            DB 1; Length 118;
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59.3%; Pred. No. 7.6e-31;
tive 19; Mismatches 25; Indels
                                                                                           29; Indels
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NON_TER 117 117
SEQUENCE 117 AA; 12993 MW; 3CF8ACE4BE447E41 CRC64;
118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
                                          57.3%; Score 375.5; DB 1, 58.5%; Pred. No. 4.3e-31; iive 17; Mismatches 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
PIR; A02039; MHMS4E.
HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUN-2002 (Rel. 41, Last annotation update)
15 heavy chain V region MOPC 104E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 AA.
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InterPro; IPR003596; Ig_v.
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Best Local Similarity 59.3%
Matches 73; Conservative
                                                                                    72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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SM00406; IGv; 1.
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                                        Query Match
Best Local Similarity
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P01756;
SEQUENCE
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HV11_MOUSE
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                                                                                                                                                                                                                                                                                                                                       "Heavy chain, variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
--- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                         MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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COMPLEMENTARITY-DETERMINING-2.
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60.2%; Pred. No. 1.3e-30;
                                          (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
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137 AA
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                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence upd
15-JUL-1999 (Rel. 38, Last annotation upd
15 heavy chain V region S43 precursor.
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  PRT;
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  STANDARD;
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                                                                                                                                       Mus musculus (Mouse)
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137
137 AA;
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                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                    Baltimore D.;
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HV11_MOUSE
P01755;
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P03980;
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HV01_MOUSE
P01745;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             20 QVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRPGQGLEWIGEINPNDGRSNY 79
                                                                                                  MEDLINE-84248078; PubMed-6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
                                                                                                                                 "Illegitimate recombination generates a class switch from C mu to C delta in an IgD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
BIR; A02033; HYMST7.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                                                                                                                                                                                                      56.3%; Score 369; DB 1; Length 138; 58.1%; Pred. No. 2.3e-30;
                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                 COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                           26; Indels
                                                                                                                                                                                                                                                                                                                                                                 15576 MW; 748157E4C6907B8E CRC64;
23-oCT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region AC38 15.3.
                    Ig heavy chain V region TEPC 1017 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 AA.
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InterPro; IPR003596; Ig_V.
InterPro; IPR004596; Ig_V.
SWART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
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                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                138 AA;
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                                                                   NCBI_TaxID=10090;
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                                                                                                                        Tucker P.W.;
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P06329;
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SEQUENCE
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Nucleic Acids Res. 814839-4840(1980).
-!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A WYELOMA THAT SECRETES IGG2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                       3; Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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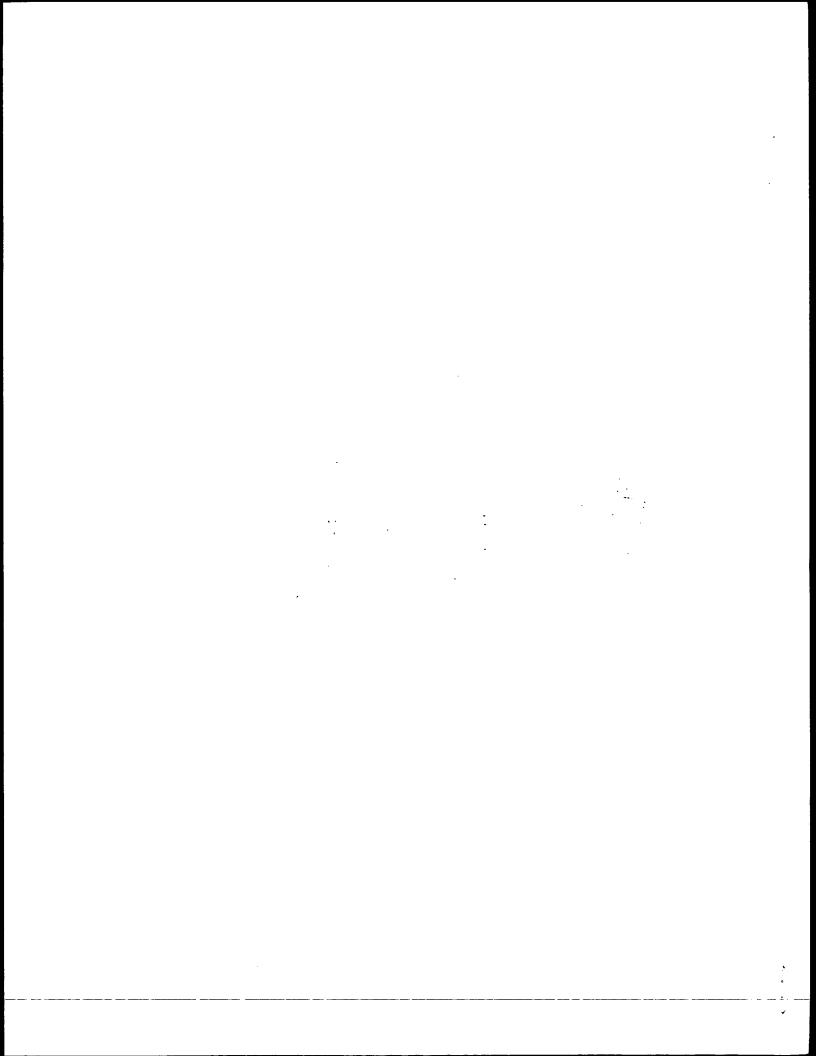
MEDLINE-81053741; PubMed-6253904;

Zakut R., Cohen J., Givol D.;

"Cloning and sequence of the CDNA corresponding to the variable region of immunoglobulin heavy chain MPCII.";

Nucleic Acids Res. 8:3591-3601(1980).
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                                                                                                                                                                                                                                                                         55.6%; Score 364.5; DB 1 56.1%; Pred. No. 5.6e-30;
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region MPC 11.
                                                                                                                                                                                                                                                                                                                     19; Mismatches
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                                                                                                                                         D SEGMENT.
J SEGMENT.
BY SIMILARITY.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR001596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Matches 69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                              120
96
120
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22
120 1
120 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
SEQUENCE FROM N.A.
MEDLINE-8222222; Pubmed-6806821;
KRAPP M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 QVQLQQSGPEVVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYNGNTSY 79
                                                                                                                                                                                                                                                                                                                                                                                                                      "Simultaneous expression of immunoglobulin mu and delta heavy chains by a cloned B-cell lymphoma: a single copy of the VH gene is shared by two adjacent CH genes "."
Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 56.9%; Pred. No. 1.8e-29;
Matches 70; Conservative 17; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V REGION BCL1.
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                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                    136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: January 6, 2003, 13:15:47
Job time: 6.21212 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin V region; Signal. siGNAL 1 19
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                    STANDARD;
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SMART; SM00406; IGv; 1.
                                                 121 VSS 123
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P01759;
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SEQUENCE
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HV15_MOUSE
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January 6, 2003, 13:10:51; Search time 23.1091 Seconds (without alignments) 1096.702 Million cell updates/sec
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655
1 QVQLVQSGAEVKKPGASVKV......NYGVYAMDYWQQGTLVTVSS 123
                                                                                                                                                                                                                                                                                                                         671580
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                     671580 seqs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
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sp_unclassified:*
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sp_mhc:*
sp_organelle:*
sp_phage:*
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length: 2000000000
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sp_rodent:*
sp_virus:*
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Maximum DB seq
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Perfect score:
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                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\*

## SUMMARIES

		æ				
Result		Query	:			
NO.	Score	Match	Match Length DB	BB :	a	Description
1	457.5	8.69	124	4	Q9UL92	Q9u192 homo sapien
7	440.5	67.3	159	4	080960	096qs0 homo sapien
m	440	67.2	468	11	Q99L31	Q99131 mus musculu
7	432	0.99	109	11	Q9JL85	Q9j185 mus musculu
'n	432	0.99	119	4	Q9UL94	Q9ul94 homo sapien
9	432	0.99	614	4	Q96GA6	Q96ga6 homo sapien
7	428	65.3	119	Ŋ	Q9GYZ2	Q9gyz2 schistosoma
80	428	65.3	125	4	Q9UL95	Q9u195 homo sapien
σ	427	65.2	146	11	092403	Q924q3 mus musculu
10	422	64.4	473	11	Q9D8L4	Q9d814 mus musculu
11	415.5	63.4	145	11	Q924R4	Q924r4 mus musculu
12	415.5	63.4	145	11	Q924R1	Q924rl mus musculu
13	412	62.9	146	11	Q924R8	Q924r8 mus musculu
14	411.5	62.8	116	4	Q9UL89	Q9u189 homo sapien
15	409.5	62.5	145	11	092406	Q924q6 mus musculu
16	408.5	62.4	145	11	092407	Q924q7 mus musculu

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099125 mus musculu 092491 mus musculu 092499 mus musculu 092499 mus musculu 092499 mus musculu 092410 mus musculu 092470 mus musculu 092497 mus musculu 0924729 homo sapien 091471 mus musculu 092473 mus musculu 092477 mus musculu 092447 mus musculu 092446 mus musculu 095104 mus musculu 095148 mus musculu 092498 mus musculu 092498 mus musculu 092448 mus musculu	AA.  update) on update) n variable region ertebrata; Euteleo Hominidae; Homo.  N.N., Berney S.M., tic carditis and n 998).  ACD2A2 CRC64;	DB 4; Lengtn e-40; 16; Indels
408.5 62.4 473 11 099125 407.5 62.2 143 11 0924P9 407.5 62.1 117 11 0924P9 405.5 61.9 145 11 0924R2 405.5 61.8 140 11 0924R2 403.5 61.6 143 11 0924R2 403.5 61.6 143 11 0924R2 403.5 61.6 142 11 0924R2 399 60.9 142 11 0924R2 399 60.9 142 11 0924R2 394.5 60.8 481 11 091WT1 394.5 60.1 145 11 0924R6 393.5 60.1 145 11 0924R6 388.5 59.5 139 11 0924R6 388.5 59.3 139 11 0924R4 388.5 59.3 114 11 0924R4 388.5 59.3 114 11 0924R4 388.5 59.3 114 11 0924R4 388.5 59.3 143 11 0924R4 388.5 59.3 143 11 0924R4 388.5 59.5 143 11 0924R4 388.5 59.6 117 11 0924R4 388.5 59.6 117 11 0924R4 388.5 59.6 117 11 0924R4 389.5 58.5 143 11 091V67 381.5 58.2 143 11 0924R5 381.5 58.2 144 11 0924Q5 380.5 88.0 144 11 0924P5	PRELIMINARY; PRT; 12  OU (TrEMBLrel. 13, Created) OU (TrEMBLrel. 13, Last sequenctive immunoglobulin heavy ch.) I (TrEMBLrel. 19, Last annota active immunoglobulin heavy ch.) Metazoa: Chordata; Craniata; Metazoa: Chordata; Craniata; Primates; Catarrhin D=9606; BUTTI39; PubMed=9614934; U.B., Van der Merwe P.L., Kali: FROM N.A. B277139; PubMed=9614934; U.B., Van der Merwe P.L., Kali: TRO01301 MADDE528.1; IPRO03066; Ig_MHC. IPRO03066; Ig_MHC. IPRO03066; Ig_MHC. IPRO03066; Ig_WHC. IPRO03596; Ig_V. IO0406; IGV; 1.  124 124 124 124 124 AA; 13580 MW; IBAAACBD	09.8%; Score imilarity 69.5%; Pred. ; Conservative 9; Mi.
	RESULT 1 Q9UL92 D Q9UL92 D Q9UL92 DT O1-MAY-20 DT O1-MAY-20 DT O1-DEC-20 DT O1-DEC-20 DT O1-DEC-20 DT O1-DEC-20 DT O1-DEC-20 DT O1-MAY-20 DT O1-DEC-20 DT O1-DEC-	Query match Best Local S Matches 91

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Malkiel S., Liao L., Cunningham M.W., Diamond B.; "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
                                                                                                                                                                                                                                                 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                      Gaps
                                                                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                  20 EVQLQQSGAELVRPGASVKLSCTASGFNIKDSLMHWVKQRPEQGLEWIGWIDPEDGETKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYDPKFQGRV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 IITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
                                                                                                                67.2%; Score 440; DB 11; Length 468; 67.5%; Pred. No. 1e-37; ive 16; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.0%; Score 432; DB 11; Length 109; 68.7%; Pred. No. 1.1e-37; tive 15; Mismatches 15; Indels (
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv: 1.
SMART; SM00410; IG_like; 1.
PROSITE; PSO0290; IG_MHC; UNKNOWN_1.
SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with cardiac myosin.";
Infect. Immun. 68:5803-5808(2000).
EMBL; AF206021; AAF65319.1; --
HSSP; PO1810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfan; PF0047; ig; 1.
SMART; SM00405; IG, 1.
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MEDLINE=20448942; PubMed=10992488;
                                                                                                                             Local Similarity 67.5% hes 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 68.7%
hes 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                                                                 Query Match
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NON_TER
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61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAM-----DY 112
               61 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYACAR-----GLYVVVPAAFSRFDY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE------GYYGNYGVYA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 SOKFOGRLTMTRDTSTSTVYMDLSSLRSDDTAVYFCAREMEITFGGAVSKGFY----YYG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches 19; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMNWVRQAPGQGPEWMGVINPSGGSARY 79
                                                                                                                                                                                                                                                                                                                                                                        Tilson M.D.;
"Homo sapiens putative microfibrillar protein with Ig-like domain 3 mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
submitted (JUN-2001) to the EMBL/GenBank/DDbJ databases.
EMBL, AV039025; AAK82649.1; -...
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 1.
SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.3%; Score 440.5; DB 4; Length 159; 64.9%; Pred. No. 2.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.,
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 901842; 7FAB.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003509; Ig.InterPro; IPR003609; Ig.InterPro; IPR003609; Ig.InterPro; IPR003609; Ig.MHC.
InterPro; IPR003006; Ig.MHC.
                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-UUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          468 AA.
                                                                                                                                                                                                                                                               Putative matrix cell adhesion molecule-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similar to RIKEN cDNA 1810060009 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 64.99
Matches 87; Conservative
                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 MDYWGQGTLVTVSS 123
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                                                               WGQGTLVTVSS 123
                                                                                              114 WGOGTLVTVSS 124
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                                                                                                                                               RESULT 2
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RESULT 7
Q9GYZ2
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Q9UL95
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                                                                                                                                                                                                                                                                                                                                                                                                                    61 AQKFQGRVTMTKDTSISTAYMELSRLRSDDTAVYYCARGGGRGLW----FDPWGQGTLVT 116
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                              Myosin-reactive autoantibodies in rheumatic carditis and normal
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                        Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                    Length 119;
                                                                                                                                                                                                                                                                                                                                       22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: PEC099851; AAH09851.1; -
InterPro; IPR000005; HTHARAC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                              NON_TER 119 119
SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67921 MW; 55EF536E77AA9BBB CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2002 (TrEMBLrel. 20, Last annotation update)
Unknown (protein for MGC:15420).
                                                                                                                                                                                                                                                                                                               66.0%; Score 432; DB 4;
70.7%; Pred. No. 1.3e-37;
tive 10; Mismatches 22,
                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035020; AAD56256.1; -.
HSSP; P01810; 2FBJ.
INCEPTO; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       614 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                            MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                       87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGc2; 2.
                                                                                                                                                                                                                                                       SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 5.
SMART; SM00408; IGc2;
                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin domain
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  614 AA;
                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                (Fragment)
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NON_TER
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                                                                                                                                                                           [etus.";
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                                                                                                                                                                                                                                                                                                                                       Matches
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DB 4; Length 614;

66.0%; Score 432;

Query Match

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                                                                                                                                       Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DPKFQGRVTITADISASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Song X.T., Feng Z.O., Guan X.H.;
"Amplification, cloning and sequence analysis of the heavy chain variable region gene of monoclonal anti-idiotypic antibody NP30 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.3%; Score 428; DB 5; Length 119; 66.7%; Pred. No. 3.3e-37; ative 17; Mismatches 20; Indels
  71.5%; Pred. No. 9.9e-37;
tive 9; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schistosoma japonicum.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288622; AAG01452.1;
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 AA; 13567 MW; BA893873FD5FA6AB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003599; 19.
InterPro; IPR003600; 19_11ke.
InterPro; IPR003006; 19_MHC.
InterPro; IPR003596; 19_V.
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PRINTS; PR01573; SUPERTUBBY.
SMART; SM00409; IG; 1.
SMART; SM00406; IGV; 1.
SMART; SM00410; IG_like; 1.
Best Local Similarity 71.5
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                         121 VSS 123
                                                                                                                                                                                                                                                    138 VSS 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fragment).
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                                                                                                                                                                                                                                                                                                                                                                    Q9GYZ2
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PRT;
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EMBL; AK007918; BAB25349.1; -...
HSSP; PO1842; FAB..
MGD; MGI:96443; Igh-1.
InterPro; IPR003599; Ig..
InterPro; IPR003500; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                               1810060009Rik protein.
IGH-1 OR 1810060009RIK.
                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047
                                                                                                                               121 VSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                        2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kozono Y., Kozono H., Azuma T., Direct Estimatican of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).", Bubmitted (ANG-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AB067797; BAB46328.1; --InterPro, IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID=9606;
                                                                                                                                                                                              "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                        65.3%; Score 428; DB 4; Length 125; 68.8%; Pred. No. 3.5e-37; Live 10; Mismatches 27; Indels
                                                                                                                                                               Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 AA; 16136 MW; CEA8DD6E1955807F CRC64;
                                                                                                                                                                                                                                                                                                                                                            125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             092403;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
WH186.2-D-J-C mu protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                    EMBL; AF035019; AAD56255.1; -.
HSSP; PO1810; ZFBJ.
HSSP; PO1810; ZFBJ.
InterPro; IPR003006; Ig_MIC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv. 1.
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                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
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                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 68.89 nes 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                            Homo sapiens (Human).
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es 81; Conserv
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                                                                                                                                                                                 Young D.C.;
                                               (Fragment).
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SEQUENCE
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Matches
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REQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=PANCREAS;

MEDLINE=21085660; PubMed=11217851;

MEDLINE=21085660; PubMed=11217851;

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino H., Adachi J., Fukuda S.,

Alazawa K., Izawa M., Nishi K., Kiyosawa H., Rodachi J., Fukuda S.,

Alazawa K., Matsuda H.A., Ashburner M., Banalao S., Casawant T.,

Radota K., Matsuda H.A., Ashburner M., Barlalov S., Casawant T.,

Radota K., Matsuda H.A., Ashburner M., Boole G., Quackenbush J.,

Radota K., Matsudo Y., Nikaido I., Pesole G., Quackenbush J.,

Radota K., Boffelli D., Suzuki R., Tomita M., Wagner I., Washio T.,

Radota M., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Ruons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Radota M., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Radota M., Rabasa M., Weitz C., Whittaker C., Wilming L.,

Wynshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Kawaji H., Toyo-Oka K., Wasegawa Y., Kawaji H., Kohtsuki S.,

Radota M., Waselli S., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                        61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
SMOSTE; PS00290; IG_MRC; UNKNOWN_1.
SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
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SEQUENCE
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SEQUENCE
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                                            20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-finity Maturation of B Cell Antigen Receptors in Response to (4-Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AB067785; BAB63270.1;
Interpo. IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.4%; Score 415.5; DB 11; Length 145; 65.0%; Pred. No. 8.7e-36; Live 17; Mismatches 23; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
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01-DEC-2001 (TrEWBLrel. 19, Last seq
01-MAR-2002 (TrEWBLrel. 20, Last ann
VH186.2-D-0-C mu protein (Fragment)
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es 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                    121 VSS 123
                                                                                                                                                                              136 VSA 138
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SEQUENCE
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Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3 Nitrophenyl) Azetyl (NP).".
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
InterPro: IPR003006; Ig_MHC.
Pfam: PF00047; ig; I.
NON_TER
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                DB 11; Length 145;
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                                                                                                                                                                                                       63.4%; Score 415.5; DB 11; Length 64.2%; Pred. No. 8.7e-36; Live 16; Mismatches 25; Indels
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63.4%; Pred. No. 2e-35;
tive 19; Mismatches 24; Indels
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067789; BAB63274.1;
InterPro; LPR003006; Ig_MHC.
                                                                                                                                                          145 AA; 15979 MW; 0162D0A26C746C04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 AA; 16216 MW; 92460F1FDF1B7538 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sen
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                                                                                                                                                                                                                                                    79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                         145
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                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 VSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIKAIN-CJUBLY,
SIKAIN-CJUBLY,
Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                      Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
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S
                                                                                                                                                                                                                                                                                                                                                                                      Score 411.5; DB 4; Length 116; Pred. No. 1.7e-35; 3; Mismatches 25; Indels 5
                                                                                                                                                                      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydroxy-3 Nitrophenyl Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067794; BAB63279.1; -...
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                               116 116 116 116 116 AM; C8F9131DE13EA898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    092406;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
                                                                                                                                                                                                                                Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035025; AAD56261.1; -.
HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003566; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                           62.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL/6;
                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                             foung D.C.;
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1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on:
January 6, 2003, 12:46:55; Search time 29:2727 Seconds (without alignments)
573.557 Million cell updates/sec

Title:
BEGUARD 10:0, Gapext 0.5
Scoring table:
BLOSUM62
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Searched:
908470
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 0%
Listing first 45 summaries
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A\_Geneseq\_101002:\*

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| SIDSZ/gcgdata/geneseq/genesegp-embl

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Mouse VLA-4 antibo	Human VLA-4 reshap	Alpha-4 integrin m	MEI-14 light chain	Humanised alpha-4	Variable region of	Mouse anti-VLA-4 a	Human MCP-3 and mu	Human IP-10 and mu	Artificial synthet
	ID	AAR81326	AAR81332	AAW22409	AAR60627	AAW22419	AAR06252	AAR81328	AAY29913	AAY29911	AAY29916
	DB	16	16	18	15	18	11	16	20	20	20
	Query re Match Length DB 1	126	126	126	128	126	128	106	359	361	374
dР	Query	100.0	100.0	100.0	93.2	91.0	91.0	83.7	79.3	79.3	78.7
	Score	680	680	680	634	619	618.5	569	539	539	535
	Result No.	-	7	m	4	S	9	7	8	6	10

Light chain variab Humanized anti-VLA Humanised alpha-4 Murine monoclonal (FRP51)-ETA fusion Anti-op54 MAb T16 Anti-op54 MAb T16	S S I I I	Ganglioside GD3 sp TF8-569 CDR-grafte Human ovarian anti Ganglioside GD3 sp Humanized 1308F VL Humanized antibody	Human/murine IL-1 Ganglloside GD3 sp Light (Kappa) chai Amino acid sequenc Ganglloside GD3 sp Anti-human CD23 5E Mouse MAD IC11 L C PXOM2. Mus muscul	Human anti-tumour Amino acid sequenc Anti-human AILIM m Amino acid sequenc Human IGFAM-13 imm Human immune respo Thrombopoietin ago Human protein sequ
AAR78970 AAR81321 AAW22412 AAR26983 AAR26983 AAW26800	AAR85495 AAR35133 AAR13658 AAR26981 AAR13050	AAB81995 AAW10233 ABP41164 AAB81996 AAR92085	AAR47207 AAB81997 AAR1259 AAY56724 AAB81993 AAW70379 AAR12237	AAY 2842 AAY 56737 AAY 56719 AAY 56301 AAB 82912 ABG 35326 AAM 1645
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## ALIGNMENTS

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Humanized antibody; leukocyte adhesion molecule; {\tt VLA-4}; therapeutle; antibody engineering.
                                                                                                                                                                     21..43
/note= "framework region 1"
44..54
/note= "complementarity determining region 1"
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                                                                                                                                                                                                                                                                          "complementarity determining region 3"
                                                                                                                                                                                                                                   /note= complementarity determining region 77..108 /note= "framework region 3"
                                                                       Mouse VLA-4 antibody 21.6 light chain variable region.
                                                                                                                                                                                                         55..69
/note= "framework region 2"
70..76
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                                                                                                                                                            /note= "signal peptide"
                                                                                                                                       Location/Qualifiers
               AAR81326 standard; Protein; 126 AA.
                                                      23-MAR-1996 (first entry)
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126; Conservative
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                                                                                                                                                                                                                             The sequence represents the mouse antibody 21.6 light chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (see AA099892) regions are linked to human constant regions in the construction of a humanized motified using PCR Primers (See AA099895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, by the amino acid present in the equivalent position of the mouse 21.6 If Chain, plannak encoding the enimeric antibodies are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GKRPRLLIHYTSALQPGIPSRFSGSGSRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                        21.6 Ig L chain. Placemids encoding the chimmeric antibodies are transfected into COS cells. The humanized antibodies are to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, amoningitis or encephalitis. The antibodies can also be used for aetecting VIA-4, for affinity purification or for generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human VLA-4 reshaped antibody 21.6 light chain variable region.
                                                                                                                                                                           leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 680; DB 16; Length 126; 100.0%; Pred. No. 2.1e-47; lve 0; Mismatches 0; Indels 0;
                                                                                                                                                                New humanised antibodies against VLA-4 - used for inhibiting
                                                                                                           Bendig MM, Jones TS, Leger OJ, Saldanha J;
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                                                                                                                                                                                                           Disclosure; Fig 1; 105pp; English.
                                                                                      (ATHE-) ATHENA NEUROSCIENCES INC
                                            95WO-US01219.
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Matches 126; Conservative
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Chain variable region against leukoyte adhesion molecule VLA-4.

Cloned cDNA sequences of mouse 21.6 VL (AAQ9888) and VH (AAQ9882)

Cloned cDNA sequences of mouse 21.6 VL (AAQ9888) and VH (AAQ9882)

Cloned cDNA sequences of mouse 21.6 VL (AAQ9888) and VH (AAQ9882)

Cof a humanized antibody against VLA-4. The 5' and 3' ends of the mouse CDNAs are modified using PCR primers (See AAQ9885-98) and then mouse cDNAs are modified using PCR primers (See AAQ9885-98) and them a kappa or gamma-1 constant regions. In the humanized light chain, amino acids 145, 149, 158 and 169 in the humanized Light chain, amino acids 145, 149, 158 and 169 in the humanized light chain, of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.
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note= "framework region 3"
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This polypeptide comprises the light chain variable region (VL) of mouse anti-alpha-4 integrin monoclonal antibody 21.6. The complementarity determining regions (CDRs) of the 21.6 VL can be incorporated into a human REI framework to produce a claimed
                                                                                                                                                                                  Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.

    for treatment of

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                                                                                    AAW22409 standard; Protein; 126 AA
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61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
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humanised 21.6 VL (see AAW22412) and a claimed humanised 21.6 antibody that is used in the manufacture of a medicament for treating a disease selected from asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin for use as a vaccine or an immunogen. It is also useful for generating didotypic antibodies. The humanised antibodies of the invention have a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is that of the MEI-14 light chain. The protein is monoclonal antibody which can be administered to treat solid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method of treating solid or cystic tumours with antibodies administering monoclonal antibody Mel-14, having Fc deleted, using injection or deposition in the cyst cavity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 680; DB 18; 100.0%; Pred. No. 2.1e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ME1-14 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zalutsky MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR60627 standard; Protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 2; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-US02724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93US-0033864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibody; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-JUN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bigner DD, Carrel S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZALU/) ZALUTSKY M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-316669/39.
N-PSDB; AAQ73537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIGN/) BIGNER D D. CARRY) CARREL S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cystic tumours.
See also AAR60626.
                                                                                                                                                                                                                                                                                                                                                                                               126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9421294-A.
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                                                                                                                                                                                                                                                                                                                                                                                                     Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR60627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARR/)
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21-NOV-1996;
                   21-NOV-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-1989;
                                                  Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP380068-A.
                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR06252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
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                                                                                    GRRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                                                                             Gaps
                                                              1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                  "21.6 complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "21.6 complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "21.6 complementarity determining region 2"
                                                                                                                                                                                                                                       Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma: atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                        ;
0
                      Score 634; DB 15; Length 128;
Pred. No. 1e-43;
3; Mismatches 5; Indels (
                                                                                                                                                                                                                       Humanised alpha-4 integrin antibody 21.6 VL version La.
                                                                                                                                                                                                                                                                                                                                                  21..126
/label= Mat_protein
/note= "VL version La (Claim 25)"
                                                                                                                                                                                                                                                                                                                                                                                          'note= "REI framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= FR4
/note= "REI framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                          "REI framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "REI framework region 3"
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                          AAW22419 standard; Protein; 126 AA.
                                                                                                                                                                                                                                                                                                                                            /label= Leader
                       93.28;
                                                                                                                                                                                                                                                                                                                                                                                                    14..54
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 70..76
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                          55..69
/label= FR2
                                                                                                                                                                                                                                                                                                                                                                                    /label= FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FR3
                                                                                                                                                                                                          (first entry)
                                     Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77..108
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                    'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                             Chimeric Mus musculus;
                                                                                                                                                                                                                                                                                                      Chimeric Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
                              Similarity
                                                                                                                                                                                                                                                                                                            Chimeric synthetic.
       128 AA;
                                                                                                                   121 TKLEIK 126
                                                                                                                                   121 TKLEIK 126
                                                                                                                                                                                                         08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9718838-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAY-1997
        Sequence
                                                                                                                                                                                         AAW22419;
                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                   Region
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                                                                                                                                                          RESULT 5
AAW22419
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This polypeptide, designated La, comprises the light chain variable region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also AAW22412). It is composed of complementarity determining regions from the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human REI framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate mouse and human DNA sequences. The humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used to produce a claimed humanised 21.6 antibody that is useful in the manufacture of a medicament for treating asthma, atherosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GKAPRILIHYTSALQPGIPSRFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIDS, dementia, diabetes, inflammatory bowel disease, rheumatorid arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukcoyte mediated lung injury. The humanised antibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                           Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.0%; Score 619; DB 18; Length 126; 90.5%; Pred. No. 1.6e-42; Live 6; Mismatches 6; Indels (
                                                                                                                                                                                                                    Leger OJ, Saldanha J, Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Variable region of murine AHT 107 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR06252 standard; protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Fig 10; 107pp; English.
                                                                                                                                     (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                      95US-0561521,
96WO-US18807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90EP-0101351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-0441702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.5 Matches 114; Conservative
                                                                                                                                                                                                                Jones ST,
                                                                                                                                                                                                                                                                                   WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 AA;
                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT74788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TKVEIK 126
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Human MCP-3 and murine scFv38 fusion protein.
region 3"
        89..96
/label= CDR3
                                                                                                                                    95WO-US01:219.
                                                                                                                                                       94US-0186269.
                                                      /label= FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 106; Conservative
                                              97..106
                                                                                                                                                                                                                                                         Inflammatory disease.
                                                                                                                                                                                                                WPI; 1995-269276/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 AA;
                                                                                                                                                       25-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-1999
                                                                                               WO9519790-A1
                                                                                                                                    25-JAN-1995;
                                                                                                                 27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY29913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
          Region
                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY29913
ID AAY2
XX
AC AAY2
XX
AC AAY2
XX
DT 17-N
XX
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 61 GKRPRLLIHYTSALQPGIPSRFSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
                                                                                                                                                                                                                                                         1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTLTCKTSQDINKFIAWYQHKP 60
                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                                              1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                    MAbs comprising mouse CH and CL constant regions whith human variable regions may be used to create mouse/human hybrid MAbs, which have a longer serum half-life. Method can be used to produce Abs against interleukin-2 receptor and tumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "mouse light chain variable complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "mouse light chain variable complementarity
determining region 2"
                                                                                    Expression vectors for producing chimeric monoclonal antibodies - which express human constant region and non-human variable region
                                                                                                                                                                                                       91.0%; Score 618.5; DB 11; Length 128; 88.2%; Pred. No. 1.8e-42; tive 12; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "mouse light chain variable framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57..88
/label= FR3
/note= "mouse light chain variable framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "mouse light chain variable framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse anti-VLA-4 antibody 21.6 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            AAR81328 standard; Protein; 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50..56
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= FR1
 89US-0301216
                    (MOLE-) MOLECULAR THERAPEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                   02-APR-1996 (first entry)
                                                                                                                                                                                                                            Matches 112; Conservative
                                                                                                                  Disclosure; ; p; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35..49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody engineering.
                                                         WPI; 1990-232892/31.
                                                                                                                                                                                                                 Sest Local Similarity
                                                                                                                                                                                      128 AA;
                                                                                                                                                                                                                                                                                                                                      |||||::
121 GTKLEVR 127
                                                                                                                                                                                                                                                                                                                           120 GTKLEIK 126
                                                                  N-PSDB; AAQ05556
24-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                AAR81328;
                                        Zerler B;
                                                                                                                                                                                      Sequence
                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain variable region (without signal sequence). Cloned cDNA CDR sequences of mouse 21.6 variable light and variable heavy regions are linked to human constant framework regions of the REI antibody for the light chain and the 2*CL antibody for the heavy chain in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mususe CDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, CLS and L69 in the human kappa LCVR framework are replaced by the amino cell present in the equivalent position of the mouse 21.6 Ig light chain. The humanized antibodies are transfected into COS colls. The humanized antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple solerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating containing the contai
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/note= "mouse light chain variable complementarity
determining region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 106;
                                                                                                                                                                                                                           /note= "mouse light chain variable framework
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The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human Muc-1; (2) human monocyte chemotactic protein-3 (MCP-3) and human Muc-1; (3) human interferon-induced protein 10 (IP-10) and human Muc-1; (4) human SPF-1 and human Muc-1; (5) human IP-10 and HIV gpl20; (6) human MCP-3 and HIV gpl20; (7) human MDC and HIV gpl20; (6) human MCP-3 and HIV gpl20; (7) human MDC and HIV gpl20; e.g. an effector I can be used for producing an immune response, e.g. an effector I cell immune response. They can also be used for treating cancer or treating or preventing HIV infection. The fusion proteins and/or nucleotide sequences for identifying unknown tumour antigen epitopes and fine ampping of Human antigen epitopes and fine ampping of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumour antigen epitopes. The present sequence represents a fusion protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                     New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
                   Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine; immune response; HIV; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.3%; Score 539; DB 20; 91.8%; Pred. No. 1.2e-35; tive 4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human IP-10 and murine scFv38 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 118-119; 142pp; English.
                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                       99WO-US05345
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Matches 101; Conservative
                                                                                                                                                                                                                                                                                                     Kwak LW, Biragyn A;
                                                                                                                                                                                                                                                                                                                                       WPI; 1999-551418/46.
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                                                                    Homo sapiens
                                                                                                                                    WO9946392-A1
                                                                                                                                                                                                     12-MAR-1999;
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                                                                                                                                                                      16-SEP-1999.
                                                                                      Mus sp.
Synthetic.
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The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human moncoyte chemotactic protein-3 (MCP-3) and human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and HIV gp120; (7) human MCP-3 and HIV gp120; (8) human MCP-3 and HIV gp120; (7) human MCP-3 and HIV gp120; (8) human SDF-1 and HIV gp120. The fusion proteins, and nucleotide sequences encoding them, can be used for producing an immune response, e.g. an effector T cell immune CC response. They are also be used for treating cancer or treating or preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in screening assays for identifying unknown tumour antigen epitopes and fine mapping of from the nucleotide for the present sequence represents a fusion protein from the nucleotide for the form the present sequence represents a fusion protein
                                                                                                                                                                                                                                                                                                                                       New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
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                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 AA;
                                                       W09946392-A1
                                                                                                                                        12-MAR-1999;
                                                                                                                                                                              12-MAR-1998;
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                                                                                               16-SEP-1999.
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Mus sp.
Synthetic.
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                                                                                                                                                                          New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.7%; Score 535; DB 20; Length 374; illarity 94.3%; Pred. No. 2.6e-35; Conservative 3; Mismatches 3; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody; heavy metal; mercury; variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Light chain variable region for monoclonal antibody 23F8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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                                                                                                                                                                                                                                                Disclosure; Page 117-118; 142pp; English.
                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                      Kwak LW, Biragyn A;
                                                                                                                                         WPI; 1999-551418/46.
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Matches 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 AA;
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 12-MAR-1999;
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Hybridoma antibodies have been produced with the spleen cells of BALB/c mouse that had received multiple injections of mercuric ions reacted with glutathione to produce a mercuric ion coordinate covalent compound which was covalently bound to keyhole limpet hemocyanin (KLH). Eight hybridomas (IFIO, 4A10, ICI), SG4, 23F8, 2D5, 5B6 and 3E8) were producing MAbs that were strongly positive against glutatione-mercuric ions but negative against glutathione without mercuric ions. RNA was isolated from hybridoma cells with guanidine isothiocyanate. First strand cDNA synthesis was catalysed by MuLv reverse transcriptase. The primers used for cDNA synthesis of the chain expressed by the hybridoma of interest, or to the 5' and of the C kappa domain. Some of the primer used for cDNA synthesis are shown in AAQ97511-097518. The primer used for cDNA synthesis of the candal region of a particular artibody polypeptide was also used for PCR amplification of that variable region, in conjunction with an appropriate V-region primer. In addition, the VH primer AAQ97518 was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences of the PCR amplified nucleotides were determined. These are given on hand a handly and the deduced AA sequences in AAR79494-R9250 so AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45 sequence listings. The descriptions in the sequence listings are
                                                                                                                                                      New polypeptide(s) which bind heavy metals, esp. mercury - derived from monoclonal antibodies, used for detecting, removing, adding or neutralising heavy metals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 75.1%; Score 510.5; DB 16; Length 107; 1 Similarity 91.6%; Pred. No. 7e-34; 98; Conservative 3; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN-LWTFGGGTKLEIK 126
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   Wylie DE;
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Lopez O, Wagner FW,
                                                                     WPI; 1995-275415/36.
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Best Local Similarity
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                                                                                                           N-PSDB; AAQ97508
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 104
                                                                               Misc-difference 45
                                                                                                                                Misc-difference 49
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                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                      The sequence encodes the humanized mouse antibody 21.6 light chain variable region, La, directed against leukocyte adhesion molecule AAQ99829. L. Cloned CDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ9982), regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' and 5' the mouse cDNAs are modified using PCR primers (See AAQ9985-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LC PK framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig L chain. Plasmids encoding the chimaric antibodies are transfected into COS cells. The humanized antibodies can be used for inhibiting adesion of a leukocyte to an endothelial and for transfing inflammatory diseases such as multipliand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell and for treating inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma: atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
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                                                                                                New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                          74.7%; Score 508; DB 16; Length 106; 88.7%; Pred. No. 1.1e-33; Live 6; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanised alpha-4 integrin antibody 21.6 VL La.
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                                                  Saldanha J;
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                                                   Leger OJ,
                                                                                                                                               Claim 9; Page 67; 105pp; English.
                          (ATHE-) ATHENA NEUROSCIENCES INC
 94US-0186269.
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                                               Bendig MM, Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric Mus musculus;
Chimeric Homo sapiens;
Chimeric synthetic.
                                                                                                                            nflammatory disease.
                                                                         WPI; 1995-269276/35.
                                                                                                                                                                                                                                                                                                                                                                                                                    106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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Region
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This polypeptide, designated La, comprises the light chain variable region (VL) of a humanised alpha-4 integrin antibody 21.6. It is composed of complementarity determining regions (CDRs) from the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human REI framework. It can be expressed in mamwallan host cells following PCR amplification and mutagenesis of appropriate fragments of mouse and human DNA sequences. The humanised 21.6 VL and a humanised 21.6 vM (see AW22413) can be used to produce a claimed humanised 21.6 antibody that is useful in the manufacture of a medicament for treating asthma, atherosclerosis,
                                                             /note= "21.6 complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "21.6 complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "21.6 complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.6 VL, important in supporting the CDR2 loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "REI Leu-103 substd by Val, more typical of human kappa light chain J region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "REI Gln-104 substd. by Glu, more typical of human kappa light chain J region"
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                                                                                                                                                                                                               /note= "REI Lys-45 is substd. by Lys of mouse
21.6 VL, important in supporting the
CDR2 loop"
                                                                                                                                                                                                                                                                                                                                                 /note= "REI Tyr-49 is substd. by His of mouse 21.6 VL, located at the binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "REI Val-58 is substd. by Ile of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "REI Thr-69 is substd. by Arg of mouse
21.6 VL, involved in antibody-antigen
binding"
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                                                                                                                                                            /note= "REI framework region 2"
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24..34
/label= CDR1
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/label= CDR2
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/label= FR4
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/label= FR2
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/label= 1
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Bernard A,
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                                                                                                                                        21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                             Antibody; light chain; kappa; variable region; K20; integrin; CD29; beta 1 subunit; humanisation; Hu-K20; immunosuppressant; T cell activation; complementarity determining region; CDR.
arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
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                                                                                                 Score 508; DB 18; Length 106;
Pred. No. 1.1e-33;
6; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                              Murine monoclonal antibody K20 kappa chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                               note= "framework region"
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/label= J_kappal
                                                                                                    74.7%;
88.7%;
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/label- CDR2
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/label= CDR1
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/label= FR2
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/label= FR1
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                                                                                                                       94; Conservative
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                                                                                                             Local Similarity
                                                                                    Sequence 106 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                      The present sequence is that of the variable region of the kappa light chain from murine monoclonal antibody K20. The antibody recognises the beta 1 subunit (CD29) of integrins and inhibits activation and proliferation of peripheral T cells induced by anti-cD3 antibodies. Monoclonal antibody K20 is a preferred target for humanisation; the humanised version may be useful as an immunosuppressant. In the humanisation process, the complementarity determining regions (CDK8) of a human antibody with framework regions 70-95% homologous to those of K20 were replaced by the K20
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/label- FLAG_peptide_and_enterokinase_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody; light chain; heavy chain; tumour; c-erbB-2; variable region; ETA.
                                                                                                                                               Humanisation of non-human immunoglobulin variable regions - for produ. of humanised antibodies, esp. K20, e.g. as an immunosuppressant
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/label= FRP5_light_chain_variable_domain
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Cervoni MF, Lefranc MP, Margaritte C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.7%; Score 508; DB 17;
89.6%; Pred. No. 1.1e-33;
iive 5; Mismatches 6;
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/label= ompA_signal_peptide
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/label= ETA_252-613
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                                                                                                                                                                                                                                                             Example 1; Fig 2A; 39pp; French.
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                                                                             WPI; 1996-162083/17
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                                                                                                        N-PSDB; AAT26849
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The sequences given in AAR26982-3 contain part of the exotoxin A sequence corresponding to positions 252-613 of the full exotoxin A sequence. These sequences are encoded by Fv(FRP5)-FTA fusion genes. The ETA sequence was used as a marker gene so that E. coli transformed expressed in E. coli and the antibodies were extracted. These recombinant antibodies can be used for the qualitative and quantitative determination of c-eTBb-2. This can be used for monitoring or in-vivo localisation of tumours overexpressing c-erbb-2.
                                                                                                                                                                                 Recombinant antibodies directed to growth factor receptor C-erbB-2 for diagnosing and treating tumours expressing C-erbB-2 e.g. breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 74.7%; Score 508; DB 13; Length 637; Best Local Similarity 86.4%; Pred. No. 6.4e-33; Matches 95; Conservative 5; Mismatches 10; Indels (
                                                                          Harwerth I, Hynes NE, Wels WS;
                                                                                                                                                                                                                                                   Disclosure; Page 53-58; 67pp; English.
   91EP-0810079.
                                                                          Hardman N,
                                      (CIBA ) CIBA GEIGY AG.
                                                                                                                         WPI; 1992-302096/37.
                                                                                                                                                                                                                       or ovarian tumours
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05-FEB-1991;
                                                                          Groner B,
Zwickl M;
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Search completed: January 6, 2003, 13:15:15 Job time: 31.2727 secs

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17 GAQCDIQMTQSPSSLSASLGGKVTLTCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76

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January 6, 2003, 13:13:21; Search time 10.4364 Seconds (without alignments) 355.228 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                               262574 seqs, 29422922 residues
                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2\_6/ptodata/1/laa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/1/laa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/1/laa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/1/laa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/laa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/laa/pcTUS\_COMB.pep:\* Issued\_Patents\_AA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 2, Appli	Sequence 15, Appl	Sequence 2, Appli	Sequence 15, Appl	Sequence 4, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 22, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 16, Appl	16,		Sequence 11, Appl		Sequence 14, Appl	Sequence 14, Appl	Sequence 5, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli		Sequence 19, Appl	Sequence 63, Appl	-	Sequence 71, Appl
QI	US-08-561-521-2	US-08-561-521-15	PCT-US95-01219-2	PCT-US95-01219-15	US-08-339-582-4	US-08-561-521-5	PCT-US95-01219-5	US-08-888-366-22	US-08-561-521-7	PCT-US95-01219-7	US-08-235-838-16	US-08-465-473B-16	US-08-235-838-11	US-08-465-473B-11	US-08-875-811-57	US-08-259-372A-14	US-08-468-671-14	US-08-458-516-5	US-08-348-548-4	PCT-US95-15716-4	US-08-236-520-2	PCT-US95-05262-2	US-09-225-322B-10	US-09-225-322B-19	US-08-480-434-63	US-08-053-451B-63	US-08-836-561-71
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% Query Match	100.0	100.0	100.0	100.0	93.2	83.7	æ	75.1	74.7	74.7	74.7	74.7	74.0	74.0	73.7	64.5	64.5	64.3	64.3	64.3	64.3	64.3	63.9	63.9	63.3	63.3	63.2
Score	089	680	680	680	634	569	269	510.5	508	508	508	508	503	503	501	438.5	438.5	437.5	437.5	437.5	437.5	437.5	434.5	434.5	430.5	430.5	429.5
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Query Match 100.0%; Score 680; DB 2; Length 126; Best Local Similarity 100.0%; Pred. No. 1.7e-59; Matches 126; Conservative 0; Mismatches 0; Indels (

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		ATION: Bendig,
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66223 66223 66224 6611 6611 6611 660 6611 660 6611 660 6611 660 660		1
$\overline{\mathbf{w}}$		1 1 2 2 2 2 4 App    L No. 5840    RAL INFORM    PLICANT:    PLICANT:    PLICANT:    PLICANT:    PLICANT:    TLE OF INV    TLE OF INV    MBR OF SEETS    COUNTY:    ZIP:    STATE:    ADDRESSEE:    ZERREE:    ZERREERREERREERREERREERREERREERREERREE
4426 426 424 423 423 4417 4417 4414 4414 4413		11-521-2 10e 2, p 10e 2, p 10e 2, p 11.521-2 11.CANT: 12.LCANT: 12
<b>4444444444444</b>		Sequence 2, Application US/08561 Septent No. 5840299 GENERAL INFORMATION: APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier J. TITLE OF INVENTION: Humanizer TITLE OF INVENTION: Humanizer TITLE OF INVENTION: Adhesion NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and TC STREET: One Market Plaza, CITY: San Francisco STREET: One Market Plaza, COUNTRY: USA ZIP: 94105 COMPUTER READABLE FORM: MEDTUM TYPE: Floppy disk COMPUTER READABLE FORM: APPLICATION NUMBER: US/08, FILING DATE: PATENTIN REGESSE CLASSIFICATION NUMBER: US/08, FILING DATE: APPLICATION NUMBER: US/08, FILING DATE: ASSUENCE TOWNER: US/08, FILING DATE: ASSUENCE TOWNER: US/08, TELEFAX: 415-543-5043 INPORMATION FOR SEQ ID NO: 2: SEGUENCE CHARACTERISTICS: LENGTH: 126 amino acids TOPOLOGY: Linear MOLECULE TYPE: protein
22288888888888888888888888888888888888		SULT 1 SULT 1 SEQUENCE Sequence Sequence APPLIA APPLIA APPLIA APPLIA APPLIA APPLIA CORR CORR CORR CORR CORR CORR CORR COR
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                                                                               1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
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APPLICANT: Bendig, Mary M.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 680; DB 2; 100.0%; Pred. No. 1.7e-59;
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APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORING SATE: NECEMBERING:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15270-14
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                                                                                                                                                                                                                                               Sequence 15, Application US/08561521
Patent No. 5840299
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELEPHONE: 415-543-9600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 126 amino acids TYPE: amino acid
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Matches 126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-561-521-15
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94105
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US-08-561-521-15
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APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 126;
                                                                                                                                                                                                                                             E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CAPPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 680; DB 5; Best Local Similarity 100.0%; Pred. No. 1.7e-59; Matches 126; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: PCT/US95/01219
25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
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                                        Sequence 2, Application PC/TUS9501219 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 152
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bendig, Mary M.
Leger, Olivier J.
Saldanha, Jose
Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 126 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Smith, William L. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-2
                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                STREET: One Market P
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                              USA
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RESULT 3
PCT-US95-01219-2
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APPLICANT:
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APPLICANT:
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us-09-155-739-2.rai

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61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.2%; Score 634; DB 1; Length 128; Best Local Similarity 93.7%; Pred. No. 5.4e-55; Matches 118; Conservative 3; Mismatches 5; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE: and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                              FILING DATE:
CLASSIPECATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,864
FILING DATE: 19-MRR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Salley, Kenneth D.
REGISTRATION NUMBER: 31,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/186,269A FILLING DATE: 25-JAN-1994
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                                                                                           APPLICATION NUMBER: US/08/339,582
                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 5405-89
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08561521; Patent No. 5840299; GENERAL INFORMATION: APPLICANT: Bendig, Mary M.
                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
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PRIOR APPLICATION DATA:
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: California
RY: USA
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRPSIQFLGLLLFWLHGAQCDIQWTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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  TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS:
                                                                                                ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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Patent No. 5558852;
GENERAL INFORMATION:
APPLICANT: Bigner, Darell D.
APPLICANT: Zalutsky, Michael R.
APPLICANT: Carrel, Stefan
TITLE OF INVENTION: METHOD OF TREATMENT;
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                       NUMBER: PCT/US95/01219
25-JAN-1995
N:
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15270-14
                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: NO. 555885zth Carolina
COUNTRY: USA
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TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                 IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-15
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MEDIUM TYPE: Floppy
                                                                                                                                             CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2: CLASSIFICATION:
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GENERAL INFORMATION:
APPLICANT: Lopez, Osvaldo
APPLICANT: Wile, Dwane E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefo
                                                                                              0; Gaps
                                                                                                                           21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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                                                83.7%; Score 569; DB 5; Length 106; 100.0%; Pred. No. 9.8e-49; Live 0; Mismatches 0; Indels
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
CITY: Minneapolis
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/888,366
FILLING DATE: 03-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRICE APPLICATION 1973

PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-2AN-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
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; Patent No. 5972656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: LENGTH: 107 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Carter, Charles G. REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-888-366-22
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                                                                  Best Local Similarity
Matches 106; Conserv
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US-08-888-366-22
          PCT-US95-01219-5
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                 83.7%; Score 569; DB 2; Length 106; 100.0%; Pred. No. 9.8e-49; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
            NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERNEC/POCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: PCT/US95/01219
25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Smith, William L. REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15, TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-560
TELEPRAX: 415-543-564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFORMATION FOR SEQ ID NO: 5:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 106; Conservative
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amino acid
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                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: STATE:
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STATE:
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1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAMYQHKPGKGPRLLIHYTSTLQPGIPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldaha, Joses
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
INUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.7%; Score 508; DB 2; Length 106; 88.7%; Pred. No. 9e-43;
                                                            81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN-LWTFGGGTKLEIK 126
                                                                                     81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Townsend and Townsend Khourie and Crew
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CURRENT APPLICATION DATA:
PILLING DATE: US/08/561,521
FILING DATE:
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9
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/186,269A
FILLING DATE: 25-JAN-1994
ATTORNEY/ACENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECHMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application PC/TUS9501219 GENERAL INFORMATION:
                                                                                                                                                                                                              Sequence 7, Application US/08561521
Patent No. 5840299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bendig, Mary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 88.79
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: One Market Pl
CITY: San Francisco
STATE: California
COUNTRY: USA
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STRANDEDNESS: si
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US-08-561-521-7
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21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.7%; Score 508; DB 5; Length 106; 88.7%; Pred. No. 9e-43; tive 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Hores, Nancy E.
APPLICANT: Horesth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Groner, Bernd
APPLICANT: Arickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGRDYTFTISSLQPEDIATYCLQYDNLWTFGGGTKVEIK 106
                                                                                                                                                                    E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
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CADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Smith, William L. REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 16, Application US/08235838
; Patent No. 5571894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
Leger, Olivier J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 7:
                         Saldanha, Jose
Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94; Conservative
                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                      COUNTRY: U:
ZIP: 94105
                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-235-838-16
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17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.7%; Score 50%; DB 2; Length 637; 86.4%; Pred. No. 7.5e-42; tive 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Hynes, Nancy E.
APPLICANT: Hardman, No. 5571894man
APPLICANT: Zwick!, Markus
APPLICANT: Zwick!, Markus
APPLICANT: Zwick!, Markus
APPLICANT: Welson Wecombinant Antibodies Specific for a TITLE OF INVENTION: Growth Factor Receptor
                                                        PRIOR PAPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pfelifer, Hesna J.
REGISTRATION NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
TELECOPHONICATION INFORMATION:
TELEPHONE: (908)522 6940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
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STREET: 7 Skyline Drive
CIIY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/235,838 FILING DATE: TBA
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08235838
Patent No. 5571894
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (908)522 6955
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
          FILING DATE: 5 June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 637 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 86.49
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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: USA
                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-465-473B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Hynes, Nancy E.
APPLICANT: Hyneverth, Ina Maria
APPLICANT: Hardman, No. 5939531man
APPLICANT: Hardman, No. 5939531man
APPLICANT: Arckl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.7%; Score 508; DB 1; Length 637; 86.4%; Pred. No. 7.5e-42; Live 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Indels
                                                                                                              COMPOTER: File Page 418.

COMPOTER: File Page 418.

COMPOTER: The PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CHENG DATE: TBA PELICATION NUMBER: US/08/235,838 FILING DATE: TBA PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/828,832 APLICATION NUMBER: US 07/828,832 PRIOR APPLICATION NUMBER: GB 91-810079.3 APPLICATION NUMBER: GB 91-810079.3 APPLICATION NUMBER: GB 91-810079.3 APPLICATION NUMBER: GB 91-810079.3 APPLICATION NUMBER: 35,129 APPLICATION NUMBER: 35,129 APPLICATION NUMBER: 36,129 REFERENCE/DOCKET NUMBER: 36,129 REPRENCE/DOCKET NUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/08465473B Patent No. 5939531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOVARTIS Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564 Morris Avenue
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 637 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 86.48 Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                               COMPUTER READABLE FORM:
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                                                                                                MEDIUM TYPE:
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US-08-465-473B-16
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COUNTRY:
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APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: NOVARTIS COTPORTION
STREET: 564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                            Query Match 74.0%; Score 503; DB 1; Length 241; Best Local Similarity 86.2%; Pred. No. 7.3e-42; Matches 94; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 GIPSRESGSGSCRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEI 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
FILING DATE: 5 June 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Pfeiffer, Hesna J.
REGISTRATION NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522_6940
                                                    4-18518/A/CIP/CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB 91-810079.3
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APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/08465473B Patent No. 5939531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 4-185
TELECOMMUNICATION INFORMATION:
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 annino acids
TYPE: annino acids
TYPE: annino acid
TYPE: annino acids
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 05-FEB-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 amino acids
                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-235-838-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901-6940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-08-465-473B-11
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245 GGGSDIQMTQSPSSLSASLGGKVTITCKASQDIKKSIAWYQHRPGKGPRLLIHYTSTLQP 304
                                                                                                                      0; Gaps
                                                                                                                                                         17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                               Length 241;
                                                                                                                                                                                                                                                              193 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEI 241
                                                                                                                                                                                                                                       77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEI 125
                                                                             Score 503; DB 2; Length 24:
Pred. No. 7.3e-42;
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Wlodawer, Alexander
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 501; DB 3;
Pred. No. 1.8e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 015280-244100US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-FEB-1998

19-FEB-1998

ON: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                             Sequence 57, Application US/08875811 Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.78;
86.48;
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 57
SEQUENCE CHARACTERISTICS:
                                                                               74.0%;
86.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 amino acids
                                                                     Query Match
Best Local Similarity 86.27
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.49
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Faris, Susan K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) MOLECULE TYPE: protein US-08-875-811-57
TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                         US-08-465-473B-11
                                                                                                                                                                                                                                                                                                                                                        US-08-875-811-57
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Search completed: January 6, 2003, 13:19:07 Job time: 11.4364 secs

According to the Pre Publication Rules, every patent application received by the United States Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months from the effective filing date. When the application is published the contents, including the sequences, will become prior art.

Two new databases have been created to hold the pre-published sequences:

Published\_Applications\_NA contains nucleic acid sequences; the search results will have the

Published\_Applications\_AA contains amino acid sequences; the search results will have the

Each pre-published application is given a unique Publication Number. An example of a Publication Number is US20021234567A1. The "US" indicates the application was a U.S. application. The first 4 digits show the calendar year the application was published. The next 7 digits represent when the application was published. This 7-digit number starts at zero at the beginning of each calendar year. Each application published is given the next number in order. The "A" indicates a utility patent application and the "1" shows that this was the first time the application had been published. If the applicants submit changes to the application, they may requests that the changed application be published again. In such instances, the "1" at the end of the number would be replaced by a "2".

Sequences in the PGPub database are public information; it is permissible to leave these


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January 6, 2003, 13:17:36; Search time 6.10909 Seconds (without alignments) 390.875 Million cell updates/sec
                                                                                                                                                                                                                                                                                                     1 MRPSIQFLGLLFWLHGAQC......YCLQYDNLWTFGGGTKLEIK 126
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                    117078 seqs, 18951520 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                        US-09-155-739-2
                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                   Perfect score:
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. (cgn2\_6/ptodata/2/pubpaa/NS09\_PUBCOMB.pep:\*
1: (cgn2\_6/ptodata/2/pubpaa/NS10\_NEW\_PUB.pep:\*
2: (cgn2\_6/ptodata/2/pubpaa/NS10\_NEW\_PUB.pep:\*
3: (cgn2\_6/ptodata/2/pubpaa/NS10\_PUBCOMB.pep:\*
4: (cgn2\_6/ptodata/2/pubpaa/NS10\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\* /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/2/pubpaa/USO8\_NEW\_PUB.pep:\*/cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

Published\_Applications\_AA:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ARIES	
SUMMA	

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Result		Query				
Q	Score	Match	Match Length DB	80	ID	Description
	490	72.1		10	US-09-229-200A-7	Sequence 7, Appli
7	482.5	71.0		10	US-09-229-200A-17	Sequence 17, Appl
m	442.5	65.1		10	US-09-859-053-30	
4	437.5	64.3		Н	US-08-779-784-21	~
S	435.5	64.0		10	US-09-740-002-24	Sequence 24, Appl
9	434.5	63.9		10	US-09-764-304-10	Sequence 10, Appl
7	434.5	63.9		10	US-09-764-304-19	Sequence 19, Appl
80	431.5	63.5		10	US-09-229-200A-11	11,
σ	431.5	63.5		10	US-09-229-200A-15	Sequence 15, Appl
10	431.5	63.5		10	US-09-229-200A-16	Sequence 16, Appl
11	420.5	61.8		10	US-09-800-729-150	Sequence 150, App
12	418.5	61.5		10	US-09-797-481-2	Sequence 2, Appli
13	418.5	61.5		10	US-09-844-736-4	Sequence 4, Appli
14	416	61.2		10	US-09-740-002-26	
15	414.5	61.0		10	US-09-855-271-26	Sequence 26, Appl
16	413.5	8.09		10	US-09-809-739-1	Sequence 1, Appli
17	413	60.7		10	US-09-056-160B-100	Sequence 100, App
18	413	60.7	491	12	US-10-011-125-2	Sequence 2, Appli
19	411.5	60.5		10	US-09-905-243-73	Sequence 73, Appl

Sequence 152, Apple Sequence 152, Apple Sequence 103, Apple Sequence 12, Apple Sequence 12, Apple Sequence 10, Apple Sequence 10, Apple Sequence 10, Apple Sequence 10, Apple Sequence 11, Apple Sequence 12, Apple Sequence 12, Apple Sequence 12, Apple Sequence 2, Appli
US-09-056-160B-15 US-09-940-166A-6 US-09-940-166A-6 US-09-056-160B-13 US-09-056-160B-12 US-09-056-160B-12 US-09-056-160B-105 US-09-090-739-10 US-09-090-739-10 US-09-153-159-2 US-09-153-159-1 US-09-056-160B-8 US-09-253-794-6 US-09-056-160B-117 US-09-056-160B-117 US-09-056-160B-117 US-09-056-160B-117 US-09-056-160B-117 US-09-99-006-158-117 US-09-056-160B-126 US-09-99-006-158-118-117 US-09-99-006-158-118-118-118-118-118-118-118-118-118
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2335 2335 2335 2335 2335 2335 2335 2335
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## ALIGNMENTS

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Length 109;
                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 08933-7003
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETIE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                  APPLICANT: Jolliffe et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

72.1%; Score 490; DB 10;
Best Local Similarity 86.1%; Pred. No. 8.8e-34;
Matches 93; Conservative 8; Mismatches 5;
                                                                                                                                                                                                                                         STREET: One Johnson & Johnson Plaza CITY: New Brunswick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: JOHN W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
TELECOMUNICATION INFORMATION:
TELEPHONE: (898) 784-3239
TELEFAX: (908) 524-2808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 13-Jan-1999
CLASSIFICATION: <Unknown>
                                      Sequence 7, Application US/09229200A
; Patent No. US20020099179A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM
                       US-09-229-200A-7
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RESULT 1
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Gaps

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Indels

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CITY: Hackensack
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                                                                                                                                                              SEQ ID NO 30
LENGTH: 236
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US-08-779-784-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                         TYPE: PRT
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APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658Aluaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTINULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 DIOMIQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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                                                                             81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW--TFGGGTKLEIK 126
                                                                                                 APPLICANT: Joliiffe et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MD STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN-LWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Johnson & Johnson
STREET: One Johnson & Johnson Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
FILING DATE: 13-Jan-1999
CLASSIFICATION: <URKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: John W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 17
                                                                                                                                                                                                               Sequence 17, Application US/09229200A Patent No. US20020099179A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (858) 784-3239
TELEFAX: (908) 524-2808
INFORMATION FOR SEC ID NO: 17
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
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Patent No. US20020102658A1
GENERAL INFORMATION:
APPLICANT: Tsuji, Takashi
                                                                                                                                                                                                                                                                                                                                                                                         New Brunswick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 87.99
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 08933-7003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                          RESULT 2
US-09-229-200A-17
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61 GKRPRLLIHYTSALQPGIPSRFSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRPSIQFLGLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rodriguez, Moses
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
                                                                                                                                                                                                                                                                                                                                                   65.1%; Score 442.5; DB 10; Length 236; 64.6%; Pred. No. 1.4e-29; tive 20; Mismatches 24; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 411 Hackensack Ave, Continental Plaza, 4th STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1199-1-001 CIPA
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR PPLICATION NUMBER: JP 2001-99508
PRIOR PELLING DATE: 2001-03-30
PRIOR PILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    David A. Jackson, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 21, Application US/08779784
; Patent No. US20020164325A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26,742
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 64.68.
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201-487-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 08-AUG-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-09-859-053-30
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USA
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US-09-764-304-19
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APPLICANT: BRAMS, PETER
APPLICANT: BRAMS, PETER
APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
FILE REPERENCE: 037003-027559
CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
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                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                     1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
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                                                                                                                                     Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Indels
                                                                                                                                                                   Indels
                                                                                                                                 Query Match 64.3%; Score 437.5; DB 1;
Best Local Similarity 67.7%; Pred. No. 2e-29;
Matches 86; Conservative 12; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.0%; Score 435.5; DB 1
64.6%; Pred. No. 5.2e-29;
tive 14; Mismatches 30
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Patent No. US20020026036A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/09740002 Patent No. US20020001798A1
INFORMATION FOR SEQ ID NO: 21:
                                 : 131 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Ver. 2.1
              SEQUENCE CHARACTERISTICS
                                                                          , MOLECULE TYPE: protein US-08-779-784-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-740-002-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-740-002-24
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LENGTH: 234
                                     LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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1 DIQMIQSPSSLSASVGDRVTITCKASPDINNYLNWYQQTPGKAPKLLIYYTSTLQPGVPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 63.5%; Score 431.5; DB 10; Length 108; Local Similarity 76.4%; Pred. No. 5.2e-29; hes 81; Conservative 11; Mismatches 13; Indels 1;
                                                                                                                                                                                                                                                                 APPLICANT: Jolliffe et al.
TITLE OF INVENTION: COI Specific Recombinant Antibody
TITLE OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
STREET: One Johnson & Johnson Plaza
CITY: New Brunswick
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 08933-7003
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Joiliffe et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
                                                                        81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 RFSGSGSGRDYSFNISNLEPEDIATYYCLOYDNL-WTFGGGTKLEI 125
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CITY: New Brunswick
STATE: NJ
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
FILING DATE: 13-Jan-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: ORT-948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: John W. Wallen, III
REGISTRATION NUMBER: 35,403
                                                                                                                                                                                                      Sequence 15, Application US/09229200A Patent No. US20020099179A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 784-3239
TELEFAX: (908) 524-2808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
8-09-299-200A-16
; Sequence 16, Application US/09229200A
; Patent No. US20020099179A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (908)
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                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: NJ
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                                                                                                                                                                                 US-09-229-200A-15
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                                                                                                                                                             RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DGTVKLLIFYSSNLHSGVPSRFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                            61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                 1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 DIOMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                   63.9%; Score 434.5; DB 10; Length 128; 66.9%; Pred. No. 3.5e-29; ive 10; Mismatches 31; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: JOILIFFE et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Johnson & Johnson
STREET: One Johnson & Johnson Plaza
CITY: New Brunswick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMDUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: -UNKNOWN>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: John W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 13-Jan-1999
CLASSIFICATION: <UDKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: (858) 784-3239
(908) 524-2808
                                                                                                                                               OTHER INFORMATION: light chain OTHER INFORMATION: variable region
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                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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SEQUENCE CHARACTERISTICS:
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                               85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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08933-7003
                                                                                                                                                                                                                                                          Local Similarity
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US-09-229-200A-11
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                                         SEQ ID NO 19
LENGTH: 128
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Matches
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                                                                                                                                                                                                                                                                                                                                          Foon, Kenneth A.
Chatterjee, Sunil K.
TITLE OF INVENTION: WORINE ANTI-IDIOTYPE ANTIBODY 341
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 61.5%; Score 418.5; DB 19
Best Local Similarity 63.0%; Pred. No. 7.8e-28;
Matches 80; Conservative 17; Mismatches 29
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FILING DATE: 27-JUL-1999
APPLICATION NUMBER: US 08/579,940
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/365,484
FILING DATE: 28-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/797,481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-797-481-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40,130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-Feb-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                  APPLICANT: Chatterjee, Malaya
Kohler, Heinz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 142 amino acids
                                                                                                                                                                                                                          Sequence 2, Application US/09797481 Patent No. US20010047083A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: CA
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                                                                       120 GTKLEIK 126
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                                                                                                                                                                                    RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 63.5%; Score 431.5; DB 10; Length 108; Local Similarity 77.4%; Pred. No. 5.2e-29; es 82; Conservative 10; Mismatches 13; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30; Indels
                                 COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDYTFTISSLQPEDIATYCLQQYDNLIFTFGQGTKLQI 106
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TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
                                                                                                                                                                 APPLICATION NUMBER: US/09/229,200A FILING DATE: 13-Jan-1999 CLASSIFICATION: <Unknown>
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CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR PILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
SOFTWARE: PALENTIN NOTE: 217
                                                                                                                                                                                                                                                    NAME: JOHN W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
TELECOMMUNICATION INFORMATION:
TELEPHONE: (658) 784-3239
TELEFAX: (908) 524-2808
INFORMATION FOR SEQ ID NO: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16
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                                                                            COMPUTER: IBM OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                         SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
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Matches 81; Conservative
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TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF CURRENT APPLICATION NUMBER: US/09/740,002 CURRENT FILING DATE: 2000-12-20 CURRENT FILING DATE: 2000-12-20 PRIOR PLING DATE: 1999-06-18 PRIOR FILING DATE: 1999-06-18 PRIOR PLILING DATE: 1999-06-07 NUMBER: UB/488,376 NUMBER OF SEQ ID NOS: 27 SOFTWARE: PATENTING DATE: 1999-06-07 NUMBER OF SEQ ID NOS: 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 QFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Bodmer, Mark W
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Emtage, John Spencer
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
FILE REFERENCE: CARP-008
CURRENT APPLICATION NUMBER: US/09/855,271
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/347,061
PRIOR FILING DATE: 1999-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.0%; Score 414.5; DB 10; Length 128; 65.6%; Pred. No. 1.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                              61.2%; Score 416; DB 10; Length 234; 63.5%; Pred. No. 2e-27; ... 16; Mismatches 30; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: No. US20020042089Alel Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 65.6%; Pred. No. 1.5e-
Matches 80; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26, Application US/09855271 Patent No. US20020042089A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 63.58
Matches 80; Conservative
             APPLICANT: MORROW, PHILLIP
                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens US-09-740-002-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TKLEIK 126
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                                                                                                                                                                                                                                                                                                                       234
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                                                                                                                                                                                                                                                                                         SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                         Foon, Kenneth A.
Chatterjee, Sunil K.
TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.5%; Score 418.5; DB 10; Length 142; 63.0%; Pred. No. 7.8e-28; Live 17; Mismatches 29; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 30414-20004.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELERA: (415) 494-0792
TELEX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/844,736
FILING DATE: 09-Apr-1997
CLASSIFICATION: <a href="https://doi.org/10.1007/10.1007/">doi.org/10.1007/</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: April 9, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Polizzi, Catherine M.
                                                                                                                                                                       APPLICANT: Chatterjee, Malaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-740-002-26
Sequence 26. Application US/09740002
Patent No. US20020001798A1
GENERAL INFORMATION:
APPLICANT: BRAMS, PETER
                                                                                                       Sequence 4, Application US/09844736
Patent No. US20020041872A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4:
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ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                         CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 80; Conserve
121 GTKLEIK 127
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                                                             RESULT 13
US-09-844-736-4
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:| Db 126 VK 127

Search completed: January 6, 2003, 13:29:30 Job time: 7.10909 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 6, 2003, 13:12:26; Search time 11.7091 Seconds (without alignments) 1034.490 Million cell updates/sec

US-09-155-739-2

680 1 MRPSIQFLGLLLFWLHGAQC.....YCLQYDNLWTFGGGTKLEIK 126 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		æ				
Result No.	Score	Query Match	Lengt	DB		Description
	. 8	. 9	f 1 1	!	809365	kappa chain -
7	n	78.7			~	kappa chain V
m	526	7			S26329	y kappa chain V
4	~	7.	106		~	kappa chain V
S	490.5	72.1	129		S52789	·
9	9	ς.			~	y light chain V
7	488	_:			PH1064	
80	476	~			E33730	y kappa
6	ä	69.3			PL0270	~
10	δ.	÷.			PL0272	y kappa
	4.	Ψ.			PL0269	
12	4	~·			PL0271	
13	453.5	'n.			S40367	Ig kappa chain V-J
14	ď.	ı.			S40334	y kappa chain -
15	4	٠.			S40365	y kappa chain -
16	ω.	65.2			S40317	g kappa chain
17	ď	٠.;			S40333	y kappa
18	442.5	65.1	131	7	S40352	Ig kappa chain V-J
19	Ξ.	_:			K1HUWK	y kappa
. 20	439.5	_;			PH1063	g light chain V
21	ന	_:			S40336	-
22					40	g kappa
23	438	÷			S42263	g kappa cha
24	۲.	<u>.</u>			Ð	g kappa cha
25	Ľ.				S52447	m
26	ζ.	٠.			S24320	
27	436.5	÷			PL0101	ι X
28	ė.	4			S52793	ы
29	435.5	4			S04574	Ig kappa chain pre

Ig kappa chain V r Ig kappa chain V-I	0 0	chain	chain	chain	chain	chain	chain	chain	chain	chain	n i edo
S11240 A49134	A34904 S14237	S43528 BH1224	S40316	S52792	S40350 S40349	KVMST1	S40348	S40314	S03521	A23986	F36025
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127	126	117	125	129	125	128	124	122	124	127	α
64.0 63.9	63.7	63.5	63.0	62.9	62.7 62.6	62.6	62.1	61.7	61.7	61.5	613
435.5 64.0 434.5 63.9	••			•		Ĭ	_	_	Ī	_	

### ALIGNMENTS

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Ig Kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S03365
R;Feddersen, R.; van Ness, B.
Nucleic Acids Res. 17, 9797-9809, 1989
A;Tille: Direct evidence for intrastrand DNA inversion of kappa immunoglobulin gene s A;Reference number: S09365; MUID:90098844; PMID:2513557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: $26330
E;Accession: $26330
J. Exp. Med: 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a proteil A;Reference number: $26309; MUID:91341421; PMID:1908510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;;
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A;Molecule type: mRNA
A;Residues: 1-104 <STA-A
A;Residues: 1-104 <STA-A
A;Cross-references: EMBL:X59185; NID:g52316; PIDN:CAA41895.1; PID:g1334063
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW-TFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 86.6%; Score 589; DB 2; Length 125; Best Local Similarity 90.6%; Pred. No. 5.9e-44; Matches 115; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                           A;Accession: S09365
A;Status: preliminary
A;Molecule type: DMA
A;Residues: 1-125 <FED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfai: heteretramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V region - mouse
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S26330
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C;Accession: S52789

C;Accession: S52789

R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Der submitted to the EMBL Data Library, March 1995

A;Description: Light chain V region gene usage restriction and peculiarities in myelo A;Reference number: S52789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ni Alternate names: Ig kappa chain V region
C. Species: Mus musculus (house nouse)
C. Species: Mus musculus (house mouse)
C. Species: John 1998
R. Stark, S.E.; Caton, A.J.
T. Exp. Med. 174, 613-624, 1991
A. Title: Antibodies that are specific for a single amino acid interchange in a proteil A. Reference number: $26309; MUD:91341421; PMID:1908510
A. Reference number: $26309; MUD:91341421; PMID:1908510
A. Residues: 1-103 <STA>
A. Residues: EMBL:X59187; NID:952318; PIDN:CAA41897.1; PID:91334064
A. Rocession: $26331
A. Mote: the sequence of residues 1-8 and the corresponding nucleic acid sequence are A. Stesidues: 1-103 <ST2>
A. Residues: 1-103 <ST2>
A. Residue
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0
                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C:Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Molecule type: mRNA
A.Residues: 1-129 <ROC>
A.Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GKRPRLLIHYTSALQPGIPSRFSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X59191; NID:952321; PIDN:CAA41901.1; PID:91334066 (S. Superfamally: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
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ilarity 87.4%; Pred. No. 1.6e-35;
Conservative 7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                            81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.1%; Score 490.5; DB 2 Best Local Similarity 72.4%; Pred. No. 1.9e-35; Matches 92; Conservative 15; Mismatches 19
                                                                                                                                                                                                                                                                      Ig kappa chain V region - human (fragment)
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Best Local Similarity
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123 GTKVEIK 129
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A; Status: preliminary
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Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989

Aritle: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A; Reference number: A33936; MUID:89282831; PMID:2471975
A; Accession: C33936
A; Sciatus: preliminary
A; Molecule type: mRNA
A; Residues: 1-106 < MBE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: 826329
R;Stark, S.E.; Caton, A.J.
A;Exp. Med: 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein A;Reference number: $26309; MUID:91341421; PMID:1908510
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C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Açession: C39336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-104 <STA>
A; Cross-references: EMBL:X59173; NID:952309; PIDN:CAA41883.1; PID:91334059
                                                                                                                                     Gaps
                                                                                                                                                                                                                                 21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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(1.3e-38; Indels
3; Indels
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                                                                                                                                     3; Indels
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Pred. No. 2.2e-39;
                                                             ch 78.7%; Score 535; DB 1 Similarity 95.2%; Pred. No. 2.2e 99; Conservative 2; Mismatches
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F;16-90/Domain: immunoglobulin homology <IMM>
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Pred. No. 1
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94.28;
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C.Species: Mus musculus (house mouse)
C.Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C.Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C.Accession: Pul0272
R.Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 262-297, 1990
A.Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A.Reference number: PL0231; MUID:90111618; PMID:2104919
                                                                     C;Accession: PLO270
C;Accession: PLO270
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PLO231; MUID:90111618; PMID:2104919
A;Accession: PLO270
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                           C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
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A; Residues: 1-107 cSHL>
A; Residues: 1-107 cSHL>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 1-5-37 Region: framework 1
F; 1-5-90, Domain: immunoglobulin homology < INMA>
F; 24-34/Region: complementarity-determining 1
                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain V region (anti-DNA, 6B8VK) - mouse (fragment)
Ig kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment)
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Best Local Similarity 85.0%; Pred. No. 2.2e-33;
Matches 91; Conservative 5; Mismatches 10
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86.0%; Pred. No. 6.7e-34;
tive 5; Mismatches 9
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F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4
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F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
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F;50-56/Region: complementarity-determining
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Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
Afritle: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unli
A;Reference number: A33730; MUID:89367325; PMID:2502260
A;Accession: E33730
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R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1064
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C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                     Ig light chain V region (clone 202.54) - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIOMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIOMTOSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60
  1 DIQMTQSPSSLSASLGGKVTFTCKASHDIKRYIAWYQHKPGKGPRLIMDYTSSLQPGIPS 60
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.8%; Score 488; DB 2; 93.8%; Pred. No. 2.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTF 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-97 <TIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-94 <LAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
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C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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C;Date: 06-Mar_1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                           CAccession: $40367
Riklein, R.; Jachau, H.G.
Riklein, R.; Jachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: $40367
A;Accession: $40367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 LLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLE 124
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R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 127;
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                                                                                                                                                                                                                                                                                        A;Molecule type: mRNÅ
A;Residues: 1-127 <KLE>
A;Cross-references: EMBL:X72477
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-132 < KLE>
A; Residues: 1-132 < KLE>
A; Residues: 1-132 < KLE>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 66.7%; Score 453.5; DB 2; Best Local Similarity 68.9%; Pred. No. 2.8e-32; Matches 84; Conservative 16; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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Pred. No. 1.4e-31;
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64.6%; Pred. No. 1...
''ve 21; Mismatches
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                                           Ig kappa chain V-J-C region - human
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                                                                        C;Accession: PL0269
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
B;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rishlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A. D. Exp. Med. 171, 265-297, 1990
A; Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A; Reference number: PL0231; MUID:90111618; PMID:2104919
A; Accession: PL0271
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Ig kappa chain V region (anti-DNA, 3E12VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain V region (anti-DNA, 2E3VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Aqcession: PLO271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1,723/Region: framework 1
F;1,6-90/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                 F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;50-56/Region: complementarity-determining 2 F;57-84/Region: framework 3 F;89-97/Region: complementarity-determining 3 F;99-107/Region: framework 4
                                                                                                                                                                                                                                                                                                                                                                                      F;24-34/Region: complementarity-determining 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 68.3%
Best Local Similarity 85.0%
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91; Conservative
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A; Residues: 1-107 <SHL>
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Best Local S
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PL0271
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RESULT 15

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Tig Rappa chain - human (Species: Homos applicates (man) (Species: Homos applicates (man) (Species: Homos applicates (man) (Species: Homos applicates) (Homos applicates)
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Search completed: January 6, 2003, 13:18:18 Job time : 12.7091 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 6, 2003, 12:48:25; Search time 6.36364 Seconds (without alignments) 821.231 Million cell updates/sec Run on:

US-09-155-739-2 680 1 MRPSIQFLGLLLFWLHGAQC......XCLQYDNLWTFGGGTKLEIK 126 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	P04431 homo sapien	mus m	P04432 homo sapien	рошо	P01638 mus musculu	homo	homo	homo	homo	homo	homo	mas m	homo	l home	mus m	homo	homo	mus m	homod	mus 1	Enm	snm s	-	homo	homo	homo	homo	homo	homo	3 homo		E mus m	P01603 homo sapien
SUMMARIES	KV1W_HUMAN	KV5E_MOUSE	KV1X_HUMAN	KV1J_HUMAN	KV5F_MOUSE	KV1B_HUMAN	KV10_HUMAN	KV1P_HUMAN	KV1Y_HUMAN	KV1A_HUMAN	KV1M_HUMAN	KV5G_MOUSE	KV4B_HUMAN	KV11_HUMAN	KV5J_MOUSE	KV1D_HUMAN	KV4C_HUMAN	KV50_MOUSE	KV1Q_HUMAN	KV5N_MOUSE	KV5K_MOUSE	KV5M_MOUSE	KV5L_MOUSE	KV1R_HUMAN	KV1C_HUMAN	KV1H_HUMAN	KV1N_HUMAN	KV1E_HUMAN	KV1V_HUMAN	KV1F_HUMAN	KV1S_HUMAN	KV5C_MOUSE	KV1K_HUMAN
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% Query Match	64.9	62.6	60.7	59.1	58.8	58.5	58.2	57.7	57.3	26.0	55.8	55.7	55.7	55.6	55.5	55.4	55.1	55.1	54.9	54.9	54.6	54.3	54.2	53.9	53.3	53.0	52.9	52.6	52.6	52.3	52.1	52.0	51.8
Score	441.5	425.5	412.5	402	$\sim$		395.5	392.5	389.5	380.5	379.5	378.5	378.5	378	377.5	377	375	374.5	373.5	373.5	371.5	369.5	368.5	366.5	362.5	360.5	359.5	357.5	357.5	355.5	354.5	353.5	352.5
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KV1L_HUMAN	KV5U_MOUSE	KV3H_HUMAN	KV3M_HUMAN	KV5H_MOUSE	KV1G_HUMAN	KV3P_MOUSE	KV5T_MOUSE	KV3L_HUMAN	KV31_MOUSE	KV5P_MOUSE	KV5Q_MOUSE
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51.5	•	51.0	51.0	50.4	50.2	50.1	49.9	49.7	49.6	49.3	49.3

## ALIGNMENTS

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121 GTKLELK 127
                                RESULT 3
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     61 GKRPRLLIHYTSALQPGIPSRFSGSGSRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGG 119
                  GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-81052342; PubMed-6776411;
Altenburger W., Steinmetz M., Zachau H.G.;
"Functional and non-functional joining in immunoglobulin light chain genes of a mouse myeloma.";
Nature 287:603-607(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.6%; Score 425.5; DB 1; Length 128; 62.2%; Pred. No. 1.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG KAPPA CHAIN V-V REGION T1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14385 MW; AFA5563D31BB7E05 CRC64;
                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-V region Tl precursor.
                                                                                                                             128 AA.
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                                                                                                                           PRT;
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SWART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; V00772; CAA24150.1; -. PIR; A01920; KVMST1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
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Matches 79; Conservative
                                                                                                                            STANDARD;
                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 AA;
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|123 GTRLEIK 129
                                                 120 GTKLEIK 126
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P01637;
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DISULFID
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                        Klobeck H.G., Combriato G., Zachau H.G.;
"Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                   13-AnG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Daudi precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X00966; CAA25478.1; ALT_TERM. PIR; A01884; K1HUDI. HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                       MEDLINE=85014148; PubMed=6091049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Ffam; PF00047; Ig; 1.
SMART; SM00406; IGv. 1.
Immunoglobulin V region; Signal.
                                                                13-AUG-1987 (Rel. 05, Created)
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                   STANDARD;
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                                                                                                                                                                Homo sapiens (Human).
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nes 78; Conserv
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                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                      KV1X_HUMAN
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P01602;
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SEQUENCE
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KV1X_HUMAN
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us-09-155-739-2.rsp

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-!- MISCELLANBOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANBOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01862; KlHUAU.
HSSP; R01607; IREI.
InterPro; IPR003006; I9_MHC.
MEDLINE=81220975; PubMed=6264318;
Pech M., Hochtl J., Schnell H., Zachau H.G.;
"Differences between germ-line and rearranged immunoglobulin V kappa coding sequences suggest a localized mutation mechanism.";
Nature 291:668-670(1981).
PIR: A01921; KVMSL6.
HSSP: P01067; IREI.
InterPro; IPR003065; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRPSIQFIGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
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Biophys. Struct. Mech. 1:139-146(1975).
-!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE
REGION OF THE KAPPA CHAIN REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schiechl H., Hilschmann N.; "Rule of antibody structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-77022433; PubMed-1234024;
Fehlhammer H., Schlifer M., Epp O., Colman P.M., Lattman E.E.,
Schwager P., Steigemann W., Schramm H.J.;
"The structure determination of the variable portion of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYD 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.8%; Score 400; DB 1; Length 115; 65.2%; Pred. No. 4e-34; 1.1ve 15; Mismatches 24; Indels
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COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY - DETERMINING - 3
                                                                                                                                                                                                                                                                                                                                                       IG KAPPA CHAIN V-V REGION L6.
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region AU.
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                                                                                                                                                                                                                                       Best Local Similaricy Articles 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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115 1
115 AA;
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P01594;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                               Bentley D.L., Rabbitts T.H.;
"Human immunoglobulin variable region genes -- DNA sequences of two V kappa genes and a pseudogene.";
Nature 288:730-733(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 MRVPAQLIGLLLLWLPGAKCDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG KAPPA CHAIN V-I REGION HK102.
FRAMEWORK-1.
COMPLEMENTARIIY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.1%; Score 402; DB 1; Length 117; 63.7%; Pred. No. 2.5e-34; ative 21; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 110 BY SIMILMAKLII.
117 117
117 AA; 12768 MW; ADIDF3A40AF1A49B CRC64;
             21.JUL-1986 (Rel. 01, Created)
21.JUL-1986 (Rel. 01, Last sequence update)
15.JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region HK102 precursor (Fragment).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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MEDLINE=81098966; Pubmed=6779204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J00245; AAA59087.1; -.
EMBL; Z00001; CAA77292.1; -.
PIR; A01882; K1H012.
HSSP; P01607; IREI.
Genew, HGNC:5741; IGKV1-5.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             >117
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SEQUENCE FROM N.A.
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P01638;
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Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967)
                                                                                                                                                                                                                                                      Query Match 58.2%; Score 395.5; DB 1;
Best Local Similarity 71.7%; Pred. No. 1.1e-33;
Matches 76; Conservative 13; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MARKER.
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01874; K1HURY.
HSSP; P80362; IWTL.
InterPro; IPR003006; I9_MHC.
InterPro; IPR003596; I9_V.
                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last_annotation update)
                  FRAMEWORK - 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain V-I region Roy.
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                                      Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1.
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                                    NCBI_TaxID=9606;
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P01608;
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"The primary structure of a crystalline monoclonal immunoglobulin Rappa-type L-chain, subgroup I (Bence-Jones protein Rej); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   **FAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=76039968; PubMed=1182131;
Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
"The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein REI refined at 2.0-A resolution.";
Biochemistry 14:4943-4952(1975).
--- MISCELLANBOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                         Gaps
                                                                                                                                                                                        21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
19 Appa chain V-I region Rei.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                         1;
                                                                                                                                                  ch 58.5%; Score 397.5; DB 1; Length 108; 1 Similarity 70.1%; Pred. No. 6.7e-34; 75; Conservative 14; Mismatches 17; Indels 1
                                                            FRAMEWORK-2,
COMPLEMENTARITY-DETERMINING-2,
                                                                                         COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.
                                                   COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PR0047; ig; 1.
SMARY; SM00406; IGV; 1.
Immunoglobulin V region; Bence-Jones protein; 3D-structure.
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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                                                                                                                                                                                                                               81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                                                                                          61 RFSGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIK 107
                                                                                                                                E8011187EE6F6FB9 CRC64;
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PIR; A01873; K1HURE.
PDB; 1REI; 17-FEB-84.
                                 protein.
                                                                                                              BY SIMILARITY
                                                                                 FRAMEWORK - 3
                                          FRAMEWORK-1
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                                 Bence-Jones
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                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=76023758; PubMed=809329;
                                                                                                                                11939 MW;
InterPro; IPR003596; Ig_v
          Pfam, PF00047; ig; 1. SMART; SMO0406; IGv; 1. Immunoglobulin V region;
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108 AA;
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P01607;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS TO 39 AND 41.
Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;
(In) Franck F., Shugar D. (eds.);
Gamma globulins: structure and function, pp.57-74, Academic Press,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York (1969).
-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 108;
COMPLEMENTARITY - DETERMINING - 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEI 125
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Indels

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21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                           1 DIQMIQSPSSLSASVGDRVITICRASQDITNYVNWFQQRPGQAPKVLIYGASILETGVPS 60
57.3%; Score 389.5; DB 1; Length 108; 67.3%; Pred. No. 4.4e-33;
                                                                                                                                                                   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                                        ; Pred. No. 4.4e-33; 18; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region AG.
Homo sapiens (Human).
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HSSP: PO1607; 1REI.
Intervero: IPR003006; Ig_MC.
Intervero: IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SWART; SW0040; IGV.
Immunoglobulin V region; Bence-Jones protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=69234734; PubMed=4893682;
                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
                                             72; Conservative
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                         Best Local Similarity
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P01593;
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                                             Matches
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                                                                                                                                                                                                                                                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCQASQDISIFLNWYQQKPGKAPKLLIYDASKLEAGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-95086080; PubMed-7993911;
Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M., Stolomon A., Stevens F.J., Schiffer M.;
"Comparison of crystal structures of two homologous proteins: structural origin of altered domain interactions in immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M., Popp R.A., Solomon A.;
"Characterization and preliminary crystallographic data on the VL-related fragment of the human kI Bence Jones protein Wat.";
J. Mol. Biol. 147:185-193(1981).
-!-MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PDB; IWTL, 01.NOV-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                  watch 57.7%; Score 392.5; DB 1; Length 108; Local Similarity 68.2%; Pred. No. 2.2e-33; Los 73; Conservative 18; Mismatches 15; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
                         FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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                                                                  FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                              COMPLEMENTARITY - DETERMINING - 3.
                                                                                                                                                                                                                                                                                                                                                                                                                      11737 MW; D9D941B3F0FAE697 CRC64;
                                                                                                                                                                                                                11782 MW; F5ACEDE5A313DF3A CRC64;
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TN -> SD (IN REF. 2).
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AA
                                                                                                                                                                       BY SIMILARITY.
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        region; Bence-Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochemistry 33:14848-14857(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-35.
MEDLINE=81267384; Pubmed=6167731;
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InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGv; 1.
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            mmunoglobulin V
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P80362;
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"The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 244:3550-3550(1969).
-i. MISCELLANEOUS: THE C. REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-i. MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 56.0%; Score 380.5; DB 1; Length 108; Local Similarity 69.2%; Pred. No. 3.7e-32; es 74; Conservative 12; Mismatches 20; Indels 1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Lay.
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SEQUENCE FROM N.A.
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                                                                                                                                                                            kappa chains.";
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P06313;
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-!- MISCELLANDOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-II KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.

-!- MISCELLANDOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

PIR; A01871; KJHULY.

HSSP; P01607; IREI.
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MEDLINE-19221900; PubMed-111146;
Seidman J.G., Max B.E., Leder P.;
A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation.";
Nature 280:370-375(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burstein Y., Schechter I.; "Amino acid sequence of the NH2-terminal extra piece segments of the precursors of mouse immunoglobulin lambdal-type and kappa-type light
                                                                                                                                                                Capra J.D., Klapper D.G.;
Complete amino acid sequence of the variable domains of two human
IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
specificities.";
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                        MEDLINE=77038198; PubMed=824717;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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Matches 71; Conservative
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                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQY-DNLWTFGG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Subgroup IV of human immunoglobulin K light chains is encoded by a
                                                                                                           MEDLINE=67056897; PubMed=4162931;
Gray W.R., Dreyer W.J., Hood L.;
"Mechanism of antibody synthesis: size differences between mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                         Science 155:465-467(1967).
-1- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOWA POLYSOMES.
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG KAPPA CHAIN V-V REGION MOPC 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN 25% OF THE MOLECULES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 55.7%; Score 378.5; DB 1; Length 130; Best Local Similarity 59.1%; Pred. No. 7.2e-32; Matches 75; Conservative 13; Mismatches 38; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLEMENTARITY - DETERMINING - 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14311 MW; SEFEOFE71D5F1BEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam, PF00047; ig; 1.
Immunoglobulin V region; Signal; Bence-Jones protein.
chains.";
Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN'1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-IV region JI precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAMEWORK-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK - 3
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Nucleic Acids Res. 13:6515-6529(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=86041853; PubMed=2997712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130
                                                                                                                                                                                                                                                                                                                                                 PIR; A01922; KVMSM4.
HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                     SEQUENCE OF 23-130.
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 FLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDI----NK-YMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bentley D.L., Rabbitts T.H.;
"Human immunoglobulin variable region genes -- DNA sequences of two
Kappa genes and a pseudogene.";
Nature 288:730-733(1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-83129397; PubMed-6402305; Bentley D.L., Rabbitts T.H.; Bentley D.L., Rabbitts T.H.; Brolution of immunoglobulin V genes: evidence indicating that recently duplicated human V kappa sequences have diverged by gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                 IG KAPPA CHAIN V-IV REGION JI. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING - 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5FB3953066744AF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region HK101 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.7%; Score 378.5; DB 1;
57.9%; Pred. No. 7.4e-32;
iive 20; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA.
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                                                                                                                                                                                                                      HSSP; P80362; 1WTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SWART; SM00406; IGv. 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14632 MW;
                                                                                                                                                                EMBL; Z00022; CAA77317.1; -. PIR; A01904; K4HUJI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 57.9 tes 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 AA;
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P01601;
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AC PO11_H
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DD 21-JUL
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C -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WYELOMA PROTEIN. R PIRS; PO1607; IRS.

R HSSP; PO1607; IRS.

R InterPro; IPR003006; Ig_W.

R Pfam; PF00047; ig; 1.

T DOMAIN I ESSART: SW00406; IGv: 1.

T DOMAIN I ESSART: SW00406; IGv: 1.

T DOMAIN I ESSART: CONDITION OF STANDOLARMAN OF S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 MRVLAQLLGLLLLCFPGARCDIQMTQSPSSLSASVGDRVTITCRARQGISSWLAWYQQKP 62
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 117;
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 378; DB 1; Length 11:
; Pred. No. 7.2e-32;
17; Mismatches 25; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-V region MOPC 173.
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SIGNAL 1 22
CHAIN 23 >117 IG
                                                                                                                                                                         EMBL; K01322; AAA58930.1; --
EMBL; K01324; AAA58932.1; --
EMBL; V00558; CAA23824.1; --
PIR; A01881; KIHU11.
PIR; A21056; A31056.
HSSP; P01607; IREI.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_V.
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Best Local Similarity 62...
Best Tocal Similarity
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Tocal Similarity
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SMART; SM00406; IGv; 1.
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P01643;
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NON_TER
SEQUENCE
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January 6, 2003, 13:10:51; Search time 23.6727 Seconds (without alignments) 1096.702 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                             671580 seqs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Database : SPTREMBL\_21:\*
1: sp\_archea:\*
2: sp\_barchea:\*
3: sp\_lungh:\*
4: sp\_lungh:\*
5: sp\_lungh:\*
6: sp\_mammal:\*
7: sp\_mhc:\*
8: sp\_organelle:\*
9: sp\_phage:\*
10: sp\_plant:\*
11: sp\_rotehrate:\*
12: sp\_virus:\*
13: sp\_virus:\*
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17: sp\_archeap:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Q8r028 mus musculu Q910e9 mus musculu Q91178 homo sapien Q99m37 mus musculu Q8w4d0 mus musculu Q8v1j0 mus musculu Q8v1j0 mus musculu Q9u185 homo sapien Q9u186 homo sapien Q9u187 mus musculu Q9j177 mus musculu Q9j178 mus musculu Q9j177 mus musculu Q9j177 mus musculu Q9j177 mus musculu Q9j180 mus musculu	Ognuwa oryccolagus Q8tbc9 homo sapien Q8te63 homo sapien Q8wuk4 homo sapien Q8wuk3 homo sapien Q9nsd6 homo sapien Q8wtu6 homo sapien Q9u182 homo sapien
08R028 09J0E9 09UL78 08YDD0 08YDD0 08YUJ0 08YUJ0 08YUJ6 09UL85 09UL85 09UL78 09UL78 09UL78 09UL78 09UL78	09NUW5 08TBC9 08TE63 08WUK4 08WUK3 09NSD6 09UL82
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238 238 238 238 238 238 238 238 238 238	233 233 237 240 107 237
4444444444444444444 @\@\@\@\@\@\@\\@\\\@\\\\\\\\\\	37.1 33.5 31.5 31.1 30.9 30.7 30.7
327.5 319.5 319.5 318 317.5 317.5 310.5 308.5 308.5 299 295.5 291.5 291.5 291.5 291.5 291.5 291.5 291.5	252.5 228 214 211.5 210 209 208.5
11112222222222222222222222222222222222	8 6 0 H G B A A A A A A A A A A A A A A A A A A

### ALIGNMENTS

RESULT 1  0921A6  TO 0921A6  TO 0921A6  TO 0921A6;  TO 0921A6;  TO 1-DEC-2001 (TrEMBLrel. 19, Created)  TO 1-DEC-2001 (TrEMBLrel. 20, Last sequence update)  TO 1-DEC-2002 (TrEMBLrel. 20, Last sequence update)  TO 1-DEC-2002 (TrEMBLrel. 20, Last sequence update)  TO 1-DEC-2002 (TrEMBLrel. 20, Last sequence update)  TO 1-DEC-2001 (TrEMBLrel. 20, Last sequence update)  Mus musculus (Mouse).  CE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  NCBI_TaxID-10090;  RN [1]   Query Match 68.8%; Score 468; DB 11; Length 241; Best Local Similarity 80.9%; Pred. No. 8e-44; Matches 89; Conservative 6; Mismatches 15; Indels 0; Gaps	QY 17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLIHYTSALQP 76	Qy 77 GIPSRESGSGSGRDYSFNISNLEPEDIATYCLQYDNLWTFGGGTKLEIK 126 	
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61 GKRPRLLIHYTSALQPGIPSRFSGSGRDYSFNISNLEPEDIATYYCLQYDN-LWTFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                   71 TSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 60.4%; Score 410.5; DB 11; Length 234; Best Local Similarity 64.6%; Pred. No. 1.8e-37; Matches 82; Conservative 14; Mismatches 30; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC015292; AAH15292.1; InterPro; IPR003006; Ig_MHC. InterPro; IPR0010865; Ribosomal_S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 234 AA; 25929 MW; BODOBOEGEB7812D2 CRC64;
                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.9 kba protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035037; AAD56273.1; -.
HSSP; PO1607; IREI.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
                                                                                                                                234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00290; IG_MHC; UNKNOWN_1.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 AA.
                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98277139; PubMed=9614934;
                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ig; 2.
                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 GTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GTKLEVK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047;
                                                                                                                                                                                                                                                                                                                                                      TISSUE-COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Young D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fetus.";
                                                                                                                                               Q91WF8;
                                                                                                                            091WF8
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                                                                                           RESULT 4
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                                                                                                              Q91WF8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GKRPRLLIHYTSALQPGIPSRFSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DGTVKLLIYTSSLHSGVPSRFSGSGSGTHYSLTISNLEPEDIATYTCQQYSQFPFTFGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 LLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHY 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LLLCFQGSRCDIQMTQTTSSLSASLGDRVTISCSGSQGIANYLNWYQQKPDGTVKLLIYY 69
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                    62.4%; Score 424.5; DB 11; Length 234; 66.1%; Pred. No. 5.2e-39; ive 11; Mismatches 31; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.7%; Score 412.5; DB 11; Length 233; 69.2%; Pred. No. 1.1e-37; Live 10; Mismatches 25; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.1e-37;
ches 25; Indels
                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC027418; AAH27418.1; -
Hypothetical protein.
SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEABI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC013496, AAH13496.1;
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 AA; 25781 MW; BIC184DA149A16EB CRC64;
                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.8 kba protein (Fragment).
                                                                    234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 AA.
                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                               NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 GTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||||||
|121 GTKLEIK 127
                                                                                                                                                                                                                                                                                        TISSUE-COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=COLON;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
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                                                                                   Q8R062;
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                                                                Q8R062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                           RESULT 2
Q8R062
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1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQRPGKVPKSLIYAASTLQSGVPS 60
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                                                                                                                                                                                                                                                                                                                                                               21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                 1 DIQLIQSPSSMYASLGERVIITCKASQDINSYLSWFQQKPGKSPKILIYRANRLVDGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                               Ouery Match 56.0%; Score 380.5; DB 11; Length 214; Best Local Similarity 67.3%; Pred. No. 3.5e-34; Matches 72; Conservative 14; Mismatches 20; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.7%; Score 378.5; DB 4; Length 108; 67.3%; Pred. No. 2.6e-34; Live 16; Mismatches 18; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                              81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                    214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035044; AAD56280.1; -.
HSSP; PO1607; IREI.
InterPro; IPR03006; Ig_MHC.
InterPro; IPR03596; Ig_v.
Pfam; PF00047; 'ig; 1.
SMART; SMO0406; IGv. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 67.34
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Fragment)
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fetus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQMIQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                               Gaps
                                                                                                                                                           21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Kappa light chain of Mab7 (Fragment).
Kappa Light chain of Mab7 (Fragment).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.
                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MBT-2002 (TrEMBLrel. 20, Last annotation update)
Anti-streptococcal/Anti-myosin immunoglobulin kappa light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98375893; PubMed-9712075; Med. SEQUENCE FROM N.A. MEDLINE-98375893; PubMed-9712075; Mard K.E., Cunningham M.W.; Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.; Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes."; J. Immunol. 161:2020-2031(1998). EMBL; U96396; AAB68785.1; -.. InterPro; IPR003006; Ig_MHC.
                                                                                            Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 56.9%; Score 387; DB 4; Length 107; Local Similarity 67.9%; Pred. No. 2.9e-35; les 72; Conservative 15; Mismatches 19; Indels
                                                                                                                             Indels
                                                                                                                                                                                                                         81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                       61 RPSGSGSGTDFTLTISSLQPEDFATYYCQOSYSTSWTFGEGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLQPEDFATYYCQOSYSTLTFGGGTKVEIK 106
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
NON_TER 1 1 1
NON_TER 108 108
SEQUENCE 108 AA; 11738 WW; C06681716C4D16F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
                                                                                          Query Match 57.3%; Score 389.5; DB 4; Best Local Similarity 68.2%; Pred. No. 1.6e-35; Matches 73; Conservative 13; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                     PRT; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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SEQUENCE
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SEQUENCE FROM N.A.
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"T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 LLIHYTSALQPGIPSRFSGSGSRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019474; ARH19474.1;
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_NHC.
61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 234 AA; 25702 MW; 102551C58ACZFA9F CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25.7 kDa protein.
                                                                                                                          234 AA
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SMART; SM00409; 1G; 2.
SMART; SM004007; IGC1; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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STRAIN-BALB/C;
MEDLINE-20448942; PubMed-10992488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Infect. Immun. 68:5803-5808(2000).
EMBL; AF206022; AAF69320.1; -.
                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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                                                                                                                                             Q8VCP0;
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Q9JL84
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54.0%; Score 367.5; DB 11; Length 127;
Best Local Similarity 59.1%; Pred. No. 5.2e-33;
Matches 75; Conservative 14; Mismatches 37; Indels 1; Gaps
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MEDLINE-99306687; PubMed-10380019;
MEDLINE-99306687; PubMed-10380019;
Tripathi P.K., Oin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
Froon K.A., Chatterjee S.K.;
"Construction and characterization of a chimeric fusion protein
consisting of an anti-idiotype antibody minicking a breast cancer-
associated antigen and the cytokine GM-CSF.";
Hybridoma 18:193-202(1999).
EMBL; AFI21; AAK55120.1; -.
InterProx. Tripath Company of the control of
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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64.8%; Score 372.5; DB 11; Length 107;
Best Local Similarity 68.2%; Pred. No. 1.2e-33;
Matches 73; Conservative 7; Mismatches 26; Indels 1;
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NON_TER 127 127
SEQUENCE 127 AA; 13794 MW; 13F61BEBBB981FA5 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Immunoglobulin light chain (Fragment).
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
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HSSP, P80362; IWTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv!
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61 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPWTFGGGTKLEIK 107

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                            Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                   Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                               Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                            53.2%; Score 362; DB 4; Length 107; 64.2%; Pred. No. 1.7e-32; Artive 15; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Pterin-mimicking anti-idiotope kappa chain variable region
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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                                                                                                                                                                                                                                                                                                                                                             107 AA; 11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                               Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035033; AAD56269.1; -.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=98277139; Pubmed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 61.7%
hes 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             68; Conservative
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                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                              107
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SEQUENCE
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Q920E6
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Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BAINC; TISSUE-SPLEEN;
MEDLINE-20183931; PubMed-10706631;
Shinohara N., Demura T., Fukuda H.;
Isolation of a vascular cell wall-specific monoclonal antibody
recognizing a cell polarity by using a phage display subtraction
method.";
                                                                                                                                                                                                                                                                            Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.0%; Score 346.5; DB 4; Length 108; 64.5%; Pred. No. 9.2e-31; Live 12; Mismatches 25; Indels 1;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                          01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 AA; 11787 MW; DB5845F19724FB4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000)
                                                                                                                                                                                                                                                                                                          Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035035; AAD56271.1; -.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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                             PRT;
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                                PRELIMINARY;
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                                                                                                                                                                                       NCBI_TaxID=9606;
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RESULT 14
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January 6, 2003, 12:46:55; Search time 32.5253 Seconds (without alignments) 573.557 Million cell updates/sec
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746
1 MKCSWVMFFLMAVVTGVNSE.....YGNYGVYAMDYWGQGTSVTV 140
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                  908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence:
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/SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1980.DAT:\*
/SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1981.DAT:\*
/SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1982.DAT:\*
/SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1983.DAT:\*
/SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1984.DAT:\*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1989.DAT:\* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001. /SIDS2/gcgdata/geneseq/genesegp-emb1/AA1989 /SIDS2/gcgdata/geneseq/genesegp-emb1/AA1990 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991 A\_Geneseq\_101002:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Mouse VLA-4 antibo	Alpha-4 integrin m	Mouse anti-VLA-4 a	Chimaeric human/mu	Variable gamma hea	Murine ONS-21 anti	V heavy chain of r	Heavy chain variab	Human Mab #117-10C	Human VLA-4 reshap
SUMMARIES	110		AAW22410	AAR81330	AAW04379	AAR11384	AAR76664	AAR41679	AAW21845	AAW63828	AAR81333
	DB	16	18	16	17	12	16	14	18	19	16
	Query e Match Length DB	140	140	123	136	140	136	136	137	138	142
dф	Query Match	100.0	100.0	86.5	84.9	84.3	83.8	79.8	79.6	79.2	78.3
	Score	746	746	645	633	629	625	595	593.5	591	584
	Result No.	-	7	m	4	5	9	7	8	6	10

Humanised al Amino acid s HWK-20 varia Humanised al Nucleotide s Nucleotide s Heavy chain Heavy chain		IBNTS / variable region. on molecule; VLA-4; therapeutic;	tide" region 1" arity determining region 1" arity determining region 2" region 3" arity determining region 2" region 4"
AAW22428 AAB07967 AAR81324 AAR81324 AAR81324 AAW22413 AAW22413 AAW310767 AAW44121 AAW44121 AAW44121 AAW44121 AAW44121 AAW44121 AAW44121 AAW44121 AAW44121	AAMY 50,744 AAR39817 AAR39817 AAR39817 AAR39818 AAR39566 AAR39566 AAR395667 AAR395617 AAY301117 AAY301117 AAY301123 AAR30123 AAR30133 AAR30133 AAR30133 AAR30133 AAR30133 AAR30133 AAR30133	ALIGNMENTS 140 AA. ight heavy var te adhesion mo	fier pep ork ork ment ork ork
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atopic dermatitis; psoriasis; myocardial ischaemia;
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                                                                                                                                                                                                                                                         The sequence represents the mouse antibody 21.6 heavy chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned CoMs sequences of mouse 21.6 VH and VL (see AAQ99889) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized heavy chain, amino acids H27, H28, H39, H30, H44 nd H71 in the human HC VR framework are replaced by the amino acid present in the equivalent position of the mouse transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to that inflammatory diseases such as multiple sclerosis. They meningitis or encephalitis. The antibodies can also be used for anti-inflammatory alseases such as multiple cerebral traumas, meningitis or encephalitis. The antibodies can also be used for anti-inflammatory diseases when the cerebral traumas, anti-inflammatory diseases such as multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADISSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis;
                                                                                                                                                                                     New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 746; DB 16; Length 140; 100.0%; Pred. No. 9.6e-60; tive 0; Mismatches 0; Indels 0.
                                                                                                                           Leger OJ, Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha-4 integrin mouse MAb 21.6 VH region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW22410 standard; Protein; 140 AA.
                                                                                                                                                                                                                                       Disclosure; Fig 2; 105pp; English.
                                                                                                  (ATHE-) ATHENA NEGROSCIENCES INC
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                                                 95WO-US01219.
                                                                          94US-0186269.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 140; Conservative
                                                                                                                         Bendig MM, Jones TS,
                                                                                                                                                 WPI; 1995-269276/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 140 AA;
                                                                                                                                                               N-PSDB; AAQ99892.
 WO9519790-A1
                                                                         25-JAN-1994;
                                                25-JAN-1995;
                       27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW22410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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This polypeptide comprises the heavy chain variable region (VH) of mouse anti-alpha-4 integrin monoclonal antibody 21.6. The mouse anti-alpha-4 integrin monoclonal antibody 21.6. The complementarity determining regions (CDRs) of the 21.6 VH can be incorporated into a human 21/28/CL framework to produce a claimed humanised 21.6 VH (see AAW22413) and a claimed humanised 21.6 VH (see AAW22413) and a claimed humanised 21.6 contibody that is used in the manufacture of a medicament for treating a disease selected from asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid dementia, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermattis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin generating idiotypic antibodies. The humanised antibodies of the invention have a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
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                                                                                                                                                                                                                                                                                                             /label= CDR1
/note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "complementarity determining region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
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acute leukocyte mediated lung injury; therapy
                                                                                                                                                                                                                                                       note= "framework region 1"
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                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                       'label= Leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= CDR3
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/label= FR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= FR4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT74760.
                                                        Mus musculus.
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                             61 EQCLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                    61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                        Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                          /label= FR4
/note= "mouse heavy light chain variable framework
                                                                                                                                                                                                                                                                                                                          /note= "mouse heavy chain variable complementarity
determining region 2"
                                                                                                                                                                                                                                                                /note= "mouse heavy chain variable complementarity
                                                                                                                                                                                                                                                                                                                                                                                    /note= "mouse heavy chain variable complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanised antibodies against VLA-4 - used for inhibiting
                                                                                                                                                                                                                                                                                                                                                       /note= "mouse heavy chain variable framework region 3"
                                                                                                                                                                                                                                   "mouse heavy chain variable framework
                                                                                                                                                                                                                                                                                             /note= "mouse heavy chain variable framework
                                                                                                                                                         Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leger OJ, Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                            determining region 3"
                                                                                                                                                                                                                                                                        determining region 1"
                                                                                                                                                                                                             Location/Qualifiers
                                                                                                              AAR81330 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                          region 4"
                                                                                                                                                                                                                                          region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                    region 2'
                                                                   121 YGNYGVYAMDYWGQGTSVTV 140
                                                           YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                              CDR3
                                                                                                                                                                                                                                                         /label- CDR1
                                                                                                                                                                                                                                                                                                                   /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95WO-US01219
                                                                                                                                                                                                                                                                                                                                                 /label= FR3
                                                                                                                                                                                                                                                                                      /label= FR2
                                                                                                                                                                                                                           /label= FR1
                                                                                                                                          02-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    .123
                                                                                                                                                                                                                                                                                                                                                                      99..112
                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bendig MM, Jones TS,
                                                                                                                                                                                 antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-269276/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-1994;
                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                        W09519790-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUL-1995
                                                                                                                            AAR81330;
                                                                                                                                                                                                              Key
Region
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                                                           121
                                                                                                       AAR81330
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The sequence represents the mouse anti-VLA-4 antibody 21.6 heavy chain variable region (without signal sequence). Cloned CDNA CDR sequences of mouse 21.6 variable light and variable heavy regions are linked to human constant framework regions of the REI antibody for the light chain and the 2*CL antibody for the heavy chain in the construction of a humanized artibody against VLA-4. The 5' and 3' ends of the mouse CDNAs are modified using PCR primers (See AAQ9895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma 1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LVCR framework are replaced by the amino contain. Plasmids encoding the chimeric antibodies are transfected into COS chain. Plasmids encoding the chimeric antibodies are transfected into COS clist. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VML-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPKFQGKATITADISSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heavy; variable region; murine; human; myeloblastoma; chimaera; monoclonal antibody; chimera; single stranded Fv region; low human antigenicity; diagnosis; treatment; cerebral tumour;
leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 86.5%; Score 645; DB 16; Length 123; Best Local Similarity 100.0%; Pred. No. 1.1e-50; Matches 121; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimaeric human/murine MAb ONS-M21 variable heavy region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..19
/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20..136
/label= mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                         Disclosure; Page 68; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW04379 standard; Protein; 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69..85
/label= CDR_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50..54
/label= CDR_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118..125
/label= CDR_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-idiotype antibodies.
                                         inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 V 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 V 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reshaped.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKCSWVMFFLLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the product of the product of the product of the heavy and is the heavy and an expected by combining light and heavy variable region DNA, from a murine anti-human myeloblastoma cell MAD, with human light and heavy variable region DNA, from a murine and heavy constant region sequences, respectively to produce chimaeric human/murine light and heavy chain DNA mols. A recombinant vector for the expression of the heavy and light chain DNA mols. Was prepd., and used to transform a host cell. The host light chain DNA mols. sepd. and connected with a peptide linker to produce a single stranded fv region. The reshaped fv region has low human antigenicity, and is therefore expected to be useful as an agent for the diagnosis and treatment of cerebral tumours,
                                                                                                                                                                      Reshaped anti-human myeloblastoma cell human antibody - has low human antigenicity, and is therefore useful for diagnosis and treatment of cerebral tumours, e.g. myeloblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAD T84.66; gamma heavy chain; carcinoembryonic antigen; CEA; human adenocarcinoma; mouse-human chimaeric antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.9%; Score 633; DB 17; Length 136;
89.3%; Pred. No. 1.5e-49;
tive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                      The present sequence is the variable heavy region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Variable gamma heavy chain of T84.66 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20..38
/label= tryptic peptide
/note= "sequenced as peptide fragment"
39..49
                                                                                                                                                                                                                           Example 2; Page 22; 45pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR11384 standard; Protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 YVN-----QDYWGQGTSVTV 134
                                                                                                       (CHUS ) CHUGAI PHARM CO LID.
                                      94JP-0285057
                                                                              93JP-0291078.
                                                               94JP-0252166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 89.3
Matches 125; Conservative
                                                                                                                                 WPI; 1996-358509/36
                                                                                                                                                                                                                                                                                                                                                                                                                               e.g. myeloblastoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 136 AA;
                                                                                                                                               N-PSDB; AAT38600
                                    18-NOV-1994;
                                                               18-OCT-1994;
                                                                              19-NOV-1993;
            02-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
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The heavy chain variable region of murine MAb 84.66 was cloned and sequenced. It was used to produce mouse V-human C antibodies with high affinity for CEA. Chimaeric murine-human anti-CEA Abs are used to diagnose human colon adenocarcinomas.

See also AAQ10834-Q10848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTVIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pUC-M21-V(H); murine; ONS-M21 antibody; chimeric protein; medulloblastoma; brain tumour; treatment; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel anti-CEA antibody - comparable to ATCC Accession No. BH 8747, produced by recombinant DNA, used in diagnosis of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.3%; Score 629; DB 12; Length 140; ilarity 87.9%; Pred. No. 3.5e-49; Conservative 6; Mismatches 9; Indels
                                                                                                                                                    /label= complementarity determining region 118..130
/label= complementarity determining region
                                                                                               50..54
/label= complementarity determining region
                                                                           /note= "sequenced as peptide fragment"
/label= tryptic peptide
_____sequenced as peptide fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine ONS-21 antibody variable heavy chain.
                                  55..59
/label= tryptic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                 Neumaier M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR76664 standard; Protein; 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 18; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 Y--VSDYAMAYWGQGTSVTV 138
                                                                                                                                                                                                                                                                                                               90WO-US04049.
                                                                                                                                                                                                                                                                                                                                                 89US-0385102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JAN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               Riggs AD,
                                                                                                                                                                                                                                                                                                                                                                                        (CITY ) CITY OF HOPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1991-073486/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 123; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ11098
                                                                                                                                                                                                                                                                                                           19-JUL-1990;
                                                                                                                                                                                                                             WO9101990-A.
                                                                                                                                                                                                                                                                                                                                                 26-JUL-1989;
                                                                                                                                                                                                                                                                        21-FEB-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                             Shively JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR76664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                      Peptide
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61 EQGLEWIGRIDPANGNTKYDPRFQGKATITADTSFNTAYLQVNSLTSEDTAVYCASGGN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                               The gene fragment encoding the V heavy chain region is used to produce a genetically engineered antibody capable of reacting specifically with feline calcivirus (FCV). The antibody can be used to treat, prevent and diagnose FCV infection. It has a broad virus-neutralising spectrum and can be used to neutralise viruses which have acquired immunity to other neutralising antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                       Anti-feline calcivirus recombinant antibody - used to treat, prevent and diagnosis infection and is safe but effective in cats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity determining region; CDR; heavy chain; treatment; variable region; murine; mouse; human; interleukin 5; IL-5; receptor; alpha chain; monoclonal antibody; hybridoma; detection; assay; diagnosis; allergic respiratory disease; chronic bronchitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.8%; Score 595; DB 14; Length 136; 82.9%; Pred. No. 3.9e-46; tive 8; Mismatches 10; Indels
               /label- Complementary Determining Region 3.
                                                                                                                                                                                                                                 Tohya Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heavy chain variable region of KM1486 antibody.
                                                                                                                                                                                                                                 Maeda H, Mikami T, Nishiyama K,
                                                                                                                                                                                             (KAGA ) CHEMO SERO THERAPEUTIC RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= sig_peptide
20..137
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                                                                                                                                                                                                                                                                                                                                                                                               Claim 1-2; Figure 3; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW21845 standard; Protein; 137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AW-----LAYWGQGTLVTV 134
                                                                                                                        93EP-0103066.
                                                                                                                                                          92JP-0079189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 82.93
Matches 116; Conservative
                                                                                                                                                                                                                                                                                      WPI; 1993-296521/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 AA;
                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ48001
                                                                                                                        26-FEB-1993;
                                                                                                                                                            28-FEB-1992;
                                                                                                                                                                                                                                                    Tokiyoshi S;
                                                                                      22-SEP-1993
                                                                                                                                                                                                                                   Kimachi K,
                                                  EP561194-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW21845;
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 Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody; feline calcivirus; FCV; neutralise; heavy chain; virus; infection; diagnosis; treatment; prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ94485 is the plasmid pUC-M21-V(H), which encodes AAR76664 the murine antibody ONS-21 variable heavy chain. The plasmid was used in the construction of an expression vector, coneg. cDNA encoding a human/murine chimeric antibody, reactive with human meduiloblastoma (a brain tumour) cells. The chimeric antibody can be used in the diagnosis and treatment of this
                                                                                                                                                                                                                                                                                                                                                           Reconstituted antibody against human medullo:blastoma cells - contains high proportion of human antibody origin and has low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V heavy chain of recombinant anti-feline calcivirus antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.8%; Score 625; DB 16; Length 136;
88.6%; Pred. No. 7.7e-49;
Live 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Complementary Determining Region 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69..86
/label= Complementary Determining Region 2.
1..19
/label= sig_peptide
20..136
/label= mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR41679 standard; Protein; 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 14; Page 59; 120pp; Japanese.
                                                                                                                                                                                                                                                                       Ohtomo T, Sato K, Tsuchiya M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 YVN-----QDYWGQGTSVTV 134
                                                                                                                                                             94WO-JP01763.
                                                                                                                                                                                                 93JP-0291078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAR-1994 (first entry)
                                                                                                                                                                                                                                   (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                           WPI; 1995-200347/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 AA;
                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ94485
                                                                                        W09514041-A1
                                                                                                                                                             19-OCT-1994;
                                                                                                                                                                                                   19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                   antigenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Sim
Matches 124;
                                                                                                                            26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR41679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease
Peptide
                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the heavy chain variable region of the murine anti-human interleukin 5 receptor alpha chain (hIL-5R alpha) monoclonal antibody (MAD) KM1486. KM1486 is produced by the hybridoma FERM BP-5651, which was prepared by immunising Balb/c mice with hIL-5R alpha, fusing splean cells obtained from the mice with mouse myeloma P3-U1 cells and screening the resultant hybridomas. The MAD can be used to detect or assay for hIL-5R alpha and cells expressing it on their surface, especially to diagnose allergic respiratory diseases, e.g. chronic bronchitis. It can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody against alpha-chain of human interleukin 5 receptor - useful for diagnosis and treatment of respiratory allergic diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Mab #117-10C heavy chain variable region protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 79.6%; Score 593.5; DB 18; Length 137; Local Similarity 82.9%; Pred. No. 5.4e-46;
                            69.85
//label= complementarity_determining_region_2
118.126
                                                                          /label= complementarity_determining_region_3
               /label= complementarity_determining_region_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Indels
                                                                                                                                                                                                                                                         Koike M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Pages 124-125; 238pp; Japanese.
                                                                                                                                                                                                                                                         Furuya A, Hanai N, Iida A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW63828 standard; Protein; 138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 -GGLRLRFFDYWGQGTTLTV 135
                                                                                                                                                                                                                           (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                96WO-JP02588.
                                                                                                                                                                                             95JP-0232384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 116; Conservative
                                                                                                                                                                                                                                                                         Takatsu K;
                                                                                                                                                                                                                                                                                                                                                                          e.g. chronic bronchitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treat such diseases.
                                                                                                                                                                                                                                                                                                WPI; 1997-202249/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 AA;
                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT73612
                                                                                                    WO9710354-A1
                                                                                                                                                                11-SEP-1996;
                                                                                                                                                                                             11-SEP-1995;
                                                                                                                                                                                                                                                                       Nakamura K,
                                                                                                                                                                                                                                                         Anazawa H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW63828;
Region
                             Region
                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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This sequence represents the human monoclonal antibody (Mab) #117-10C

heavy chain variable region which is used in a method involved in

neutralising IL-18 or to treat autoimmune diseases or as an

meutralising IL-18 or to treat autoimmune diseases or as an

immuosuppressant using anti-IL-18 antibodies which can inhibit IL-18

Such antibodies can also be used to detect the IL-18 receptor protein

(labelled with an enzyme or a radioactive or fluorescent substance). The

protein is used to treat e.g. graft rejection, pernicious anaemia,

catrophic gastritis, insulin-resistant diabetes, Wegener granulomatosis,

discoid lupus erythematosis, ulcerative colitis, cold-agglutinin-relating

diseases, Goodpastures syndrome, primary biliary cirrhosis, sympathetic

cophrhalmitis, hyperthyroidism, juvenile onset type diabetes, Sjogren

cyptrome, autoimmune hepatitis, autoimmune haemolytic anaemia, myasthenia

cold haemoglobhurala, polymyositis, periarteritis nodosa, multiple

cold haemoglobhurala, polymyositis, periarteritis nodosa, multiple

cold haemoglobhurala, polymyositis, periarteritis nodosa, multiple

cold haemoglobhurala, polymyositis, periarteritis saleadow's disease,

cold haemoglobhurala, polymyositis, periarteritis of salease,

cold haemoglobhurala, polymyositis, periarteritis andensa, and itsple

cold haemoglobhurala, chronic hypoiditis, hedgkii's disease,

cold haemoglobhurala, periare, chronic thyroiditis, Hedgkii's disease,

arthritis, rheumatopyra, chronic thyroiditis, Hodgkii's disease,

arthritis, rheumatopyra, organic naemis, mased,

arthritis, rheumatopyra, organic haemorrhagica, and sease,

arthritis, rheumatopyra, organic properservance and polymyosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New interleukin-18 receptor protein used to inhibit interleukin-18, to treat autoimmune disease and as immunosuppressant - and new monoclonal antibody and hybridoma used to detect interleukin -18
                                                                                                         20..138
/label= Mab 117-10C heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma, atopic dermatitis, allergic nastitis, pollinosis, apitoxin-allergy and septic shock resulting from production or administration of excessive gamma interferon (IFN-gamma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.2%; Score 591; DB 19; Length 138; 83.0%; Pred. No. 9.1e-46; tive 4; Mismatches 14; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunikata T, Kurimoto M, Torigoe K, Ushio S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3.3a; Page 22; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
                                            Location/Qualifiers
                                                                 1..19
/label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 YG-NYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 YGAGFG----YWGOGTLVTV 136
                                                                                                                                                                                                                                                                                                        97JP-0215490.
96JP-0356426.
97JP-0052526.
97JP-0163490.
                                                                                                                                                                                                                                                                   97EP-0310555.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-335317/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV44000
Homo sapiens,
                                                                                                                                                                                                                                                              23-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                          06-JUN-1997;
                                                                                                                                                                                                                                                                                                                                  26-DEC-1996;
                                                                                                                                                                        EP850952-A1
                                                                                                                                                                                                                    01-JUL-1998
                                                                                                                                                                                                                                                                                                                                                       21-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                               Peptide
                                                                                                             Protein
g
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Sequence 142 AA;

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The sequence represents the human reshaped antibody 21.6 heavy chain variable region against leukocyte adhesion molecule VLA-4.

Cloned cDNA sequences of mouse 21.6 VH (AAQ9983) and VL (AAQ99889) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human caps H17, H28, H29, H30, H44 and H71 in the humanized heavy chain, amino acids H17, H28, H29, H30, H44 and H71 in the human HC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig H chain. Plasmids encoding the chimeric antibodies can be used to inhibit adhesion of a leukocyte to an artibodies can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used in the treatment of stroke, also be used in the treatment of stroke, also be used in the treatment of stroke.
                                                                                                                                             Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                 Human VLA-4 reshaped antibody 21.6 light heavy variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                               "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "complementarity determining region 3"
132..142
                                                                                                                                                                                                                                                                                                                                                                          "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sendiq MM, Jones TS, Leger OJ, Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "framework region 4"
                                                                                                                                                                                                                                                                                  "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                       "framework region 3"
                                                                                                                                                                                                                                                                                                                                             "framework region 2"
                                                                                                                                                                                                                                                      "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qenerating anti-idiotype antibodies.
                                                                                                                                                                                                                       .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 11; 105pp; English.
                             AAR81333 standard; Protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-0186269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95WO-US01219.
                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           /note= "f
118..131
                                                                                                                                                                                                                                                                                                                                                                                          86..117
                                                                                                                                                                                                                                                                                                                  /note=
55..68
                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                         'note=
                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory disease.
                                                                                                                                                                antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-269276/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ99894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9519790-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-1994;
                                                                                                                                                                                              Homo sapiens
                                                                                      23-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JUL-1995
                                                           AAR81333;
                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                       Region
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RESULT 10
               AAR81333
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61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADISSNTAYLQLSSLISEDTAVYFCAREGY 120
                       Gaps
                                                        1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= CDR3
/note= "21.6 complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "21.6 complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "21.6 complementarity determining region 2"
                                                                                                                                                                                                                                                                                                         Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                       ö
Score 584; DB 16; Length 142;
Pred. No. 4e-45;
5; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                       Humanised alpha-4 integrin antibody 21.6 VL version Ha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= FR4
/note= "21/28'CL framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "21/28'CL framework region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "21/28'CL framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "21/28'CL framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20..142
/label- Mat_protein
/.ore= "VH version Ha (Claim 25)"
                       15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                    AAW22428 standard; Protein; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= Leader
                                                                                                                                                    121 YGNYGVYAMDYWGQGTLVTV 140
                                                                                                                                      121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68..85
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50..55
/label= CDR1
 78.3%;
ilarity 77.1%;
Conservative 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55..67
/label= FR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                                                          Chimeric Mus musculus;
Chimeric Homo sapiens;
Chimeric synthetic.
              Similarity
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               Local Sim
                                                                                                                                                                                                                                           AAW22428;
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
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96WO-US18807

21-NOV-1996;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                         This polypeptide, designated Ha, comprises the heavy chain variable region (VH) of a humanised alpha-4 integrin antibody 21.6 (see also AAM22413). It is composed of complementarity determining regions from the VH region (see AAW22410) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human 21/28 CL framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate mouse and human DNA sequences. The mutagenesis of appropriate mouse and human bNA sequences. The mutagenesis of appropriate mouse and human bNA sequences. The mutagenesis of appropriate following PCR amplification and humanised 21.6 VH (see AAW22412) can be used to produce a claimed humanised 21.6 antibody that is useful in the manufacture of a medicammatory bowel disease, rheumour arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, archic dermattis, sportasis, mycoardial arthritis, and acute leukcoyte mediated lung injury. The humanised antibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody IFI; B7 molecule; B7; humanised immunoglobulin; autoimmune disease; infectious disease; inflammatory disorder; systemic lupus erythematosus; diabetes mellitus; insulitis; asthma; arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis; multiple sclerosis; transplant rejection; proliferative disease; leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia; applastic anaemia; myeloid dysplasia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of heavy chain variable region of 1F1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                          Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Owery Match 78.3%; Score 584; DB 18; Length 142; Best Local Similarity 77.1%; Pred. No. 4e-45; Matches 108; Conservative 15; Mismatches 17; Indels
                                                                      Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB07967 standard; Protein; 135 AA.
                                                                                                                                                                                     Example 6; Fig 11; 107pp; English.
                                           (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YGNYGVYAMDYWGQGTLVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 YGNYGVYAMDYWGQGTSVTV 140
               95US-0561521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-NOV-2000 (first entry)
                                                                                                WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 AA;
                                                                                                                N-PSDB; AAT74789
               21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB07967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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The present sequence represents the heavy chain variable region of the murine antibody IF1. The antibody has a binding specificity to B7 molecules. The antibody is used to construct humanized immunoglobulins, which comprise an antigen binding region of non-human origin and a bortion of a human immunoglobulin. The humanized immunoglobulins are useful for treating autoimmune diseases, infectious diseases, inflammatory disorders, systemic lupus erythematosus, diabetes inflammatory dermatitis, asthma, arthritis, inflammatory bowel disease, also useful for treating a transplant recipient or preventing transplant recipient, and multiple sclerosis. The immunoglobulins are also useful for treating a transplant recipient, and treating proliferative disease (leukemia, lymphoma and cancer), anaemia (sickle-cell amemia, disease thalassemia and aplastic aneamia), inborn errors of metabolism, congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanized immunoglobulin having a binding specificity to B7-1 (derived from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules, modulates immune responses and can therefore treat e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EQGLEWIGWIDPENGNTLYDPKFQGKASITADTSSNTAYLQLSSLTSEDTAVYYCAREGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goldman S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70...5
118..124
/note= "complementarity determining region 1"
/note= "complementarity determining region 1"
                                                                                                      "complementarity determining region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Celniker AC, Collins M,
Rup B, Veldman GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.3%; Score 576.5; DB 21; Length 80.7%; Pred. No. 1.8e-44; Indels ive 6; Mismatches 14; Indels
/note= "signal peptide"
20.135
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 8; Fig 6A; 162pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carreno B,
O'hara D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infectious diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0249011.
99US-0339596.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 113; Conservative
                                                                                                                                     69..85
                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-524532/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Knight A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vasquez M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-1999;
                                                                                                                                                                                                                                                                                                                       17-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gray GS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                         Protein
                                                                               Region
                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CO MS,
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ID AAR9
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AC AAR9
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ARM95946-R95948 represent sequences for variable regions of an antibody produced by the hybridoma cell line HNK-20. This sequence represents the actioned with a cell line, that produces IgA sequence represents in the action of respiratory syncytial virus (RSV). The DNA encoding glycoprotein of respiratory syncytial virus (RSV). The DNA encoding untranslated region of the variable region, and for the intromovanteem of the rearranged J region (see AAT30459-T30545 for primer sequences). The DNA encoding these sequences can be inserted into vectors containing heterologous (such as human) constant region genes, for the production of chimeric and isotype-switched antibodies. The antibodies are useful in the treatment and diagnosis of infection by RSV, such as concaining the variable region genes can be isotated without producing as a template, variable region genes can be isotated without producing the reagments that have to be adapted for recombinant antibody expression.
                                                                                          Antibody; HNK-20; variable heavy chain; hybridoma; murine; IgA; mouse; F glycoprotein; respiratory syncytial virus; RSV; constant region gene; chimeric antibody; isotype-switched antibody; therapy; infection; human; pneumonia; bronchiolitis; animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Also, by using the genomic DNA, no knowledge of the DNA sequence encoding the target variable region is required. Chimeric antibodies produced from these proteins, that contain the constant region of the host being treated, are less likely to cause adverse immune reactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.5%; Score 570.5; DB 17; Length 137; 81.4%; Pred. No. 6.4e-44; tive 6; Mismatches 15; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding variable region of antibody \ensuremath{\mathsf{HNK-20}} - for treating respiratory syncytial virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; Fig 5d; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YGNYGVYAMDYWGQGTSVTV 140
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                                                                                                                                                                                                                                                                                                                       95WO-US15716.
                                                           HNK-20 variable heavy chain.
                                                                                                                                                                                                                                                                                                                                                             94US-0348548
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Matches 114; Conservative
                  10-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Berdoz J, Kraehenbuhl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-286826/29.
                                                                                                                                                                                                                                                                                                                                                                                                        ORAV-) ORAVAX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT30458
                                                                                                                                                                                                                                         WO9616974-A1.
                                                                                                                                                                                                      Mus musculus.
                                                                                                                                                                                                                                                                                                                          01-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                01-DEC-1994;
                                                                                                                                                                                                                                                                                  06-JUN-1996
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The sequence encodes the mouse antibody 21.6 heavy chain variable region. Ha, directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VN (AAQ99889 and AAQ99892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into constant regions. In the humanized light chain, amino acids L45. L58 and L69 in the humanized light chain, amino acids L45. L88 and L69 in the humanized light chain, amino acids research in the equivalent position of the mouse cransfected into COS cells. The humanized antibodies are transfected into COS cells. The humanized antibodies can be used for inhibiting adhesion of a leukocyte to an endothelial cell and contracting inflammatory diseases such as multiple sclerosis. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                   Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.9%; Score 544; DB 16; Length 123; 82.6%; Pred. No. 1.4e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Mismatches
AAR81323 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 69; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                Leger OJ,
                                                                                                                                                                                                                                                                                                                                                               (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                           94US-0186269.
                                                                                                                                                                                                                                                                                           95WO-US01219.
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Best Local Similarity 82.69
Matches 100; Conservative
                                                                  02-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-idiotype antibodies.
                                                                                                                                                       antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                  Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammatory disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 AA;
                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                               25-JAN-1994;
                                                                                                                                                                                                                                                                                           25-JAN-1995;
                                                                                                                                                                                                                          W09519790-A1
                                                                                                                                                                                                                                                          27-JUL-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                  Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                  AAR81323;
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RESULT 15 AAB07969

RESULT 14 AAR81323 ij

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The present sequence represents the heavy chain variable region of the humanised murine antibody IP1. The antibody has a binding specificity to by molecules. The antibody is used to construct humanized immunoglobulins, which comprise an antigen binding region of non-human immunoglobulins, which comprise an antigen binding region of non-human immunoglobulins are useful for treating autoimmune diseases, infectious diseases, inflammatory disorders, systemic lupus erythematosus, diabetes inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are also useful for treating a transplant recipient, and treating proliferative disease (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia, thanbasemia and aplastic anaemia), inborn errors of metabolism, congenital immunodeficiency diseases, and mysloid dysplasia syndrome.
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135 AA;

Seguence

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autoimmune disease; infectious disease; inflammatory disorder; systemic lupus erythematosus; diabetes mellitus; insulitis; asthma; arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis; multiple sclerosis; transplant rejection; proliferative disease; leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia; aplastic anaemia; myeloid dysplasia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanized immunoglobulin having a binding specificity to B7-1 (derived from ATCC CRL-12524) molecules, modulates immune responses and can therefore treat e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Celniker AC, Collins M, Goldman S;
Rup B, Veldman GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "complementarity determining region 1" 69..85 /note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118..124
/note= "complementarity determining region 1"
                                                                                                                                 A heavy chain variable region of humanised 1F1 antibody.
                                                                                                                                                                           B7 molecule; B7; humanised immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "signal peptide"
AAB07969 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 10; Fig 7A; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carreno B,
O'hara D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infectious diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0249011
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                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GS, Knight A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-524532/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vasquez M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAA59698
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                                                                                                                                                                                Antibody 3D1;
                                                                                                                                                                                                                                                                                                                                                                                 Mus sp.
Homo sapiens.
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24-JUN-1999;
                                                                                    14-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                            AAB07969;
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Gray GS
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61 GGGLEWICWIDPENGNTLYDPKFGGKATITADTSTSTAYMELSSLRSEDTAVYYCAREGL 120
                                                                                                                                                       EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                          7; Gaps
                                                                                                1 MKCSWVMFFLMAVVIGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
  72.3%; Score 539.5; DB 21; Length 135; 75.0%; Pred. No. 3.9e-41; ive 11; Mismatches 17; Indels 7;
                                                                                                                                                                                                                                                                                                                                     completed: January 6, 2003, 13:15:16
                                                                                                                                                                                                                                  121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                         F-----FAYWGOGTLVTV 133
                  Best Local Similarity 75.0%
Matches 105; Conservative
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Query Match
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GenCore version 5.1.3

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2003, 13:13:21; Search time 11.596 Seconds

(without alignments)
355.228 Million cell updates/sec
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355.228 Million cell updates/:
Title: US-09-155-739-4
Perfect score: 746
Sequence: 1 MKCSWVMFFLMAVVTGVNSE.....YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Total number of hits satisfying chosen parameters: 262574

262574 seqs, 29422922 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : Issued\_Patents\_AA:\*
1: \cgn2\_6/ptodata1/liaa/5A\_COMB.pep:\*
2: \cgn2\_6/ptodata1/liaa/5B\_COMB.pep:\*
3: \cgn2\_6/ptodata1/liaa/6A\_COMB.pep:\*
4: \cgn2\_6/ptodata1/liaa/6B\_COMB.pep:\*
5: \cgn2\_6/ptodata1/liaa/PGPCUS\_COMB.pep:\*
6: \cgn2\_6/ptodata1/liaa/PCPUS\_COMB.pep:\*
6: \cgn2\_6/ptodata1/liaa/PCPUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		App11	Appli	Appli	Appli	Appl	Appli	Appl	Appl	Appl '	, Appl	, Appl	Appli	Appli		, Appl	Appli	Appli	Appli	Appli	, Appl	Appli	, Appl	Appli	Appli	Appli	Appli	Appli
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	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
	Π	US-08-561-521-4	PCT-US95-01219-4	us-08-561-521-9	PCT-US95-01219-9	US-08-646-265A-29	US-08-024-253-2	US-08-836-561-31	US-08-561-521-17	PCT-US95-01219-17	US-08-561-521-44	PCT-US95-01219-44	US-08-348-548-8	PCT-US95-15716-8	US-08-561-521-11	PCT-US95-01219-11	US-07-934-373C-6	US-08-437-642B-6	US-08-146-206C-6	PCT-US93-07832-6	US-08-871-488A-15	US-08-822-830B-2	US-08-822-830B-13	US-08-950-660-2	PCT-US93-00030-2	PCT-US93-00924-2	US-08-603-024-2	US-08-253-877C-8
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	Query Match Length	140	140	123	123	136	136	137	142	142	125	125	136	136	123	123	120	120	120	120	120	121	121	120	120	120	138	139
dР	Query Match	100.0	100.0	86.5	86.5	84.9	79.8	9.62	78.3	78.3	75.3	75.3	74.3	74.3	72.9	72.9	70.8	70.8	70.8	70.8	6.69	69.3	68.8	68.5	68.5	68.5	67.8	67.8
	Score	746	746	645	645	633	595	593.5	584	584	562	562	554	554	544	544	528.5	528.5	528.5	528.5	521.5	516	513	511	511	511	505.5	505.5
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Gaps

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Query Match 100.0%; Score 746; DB 2; Length 140; Best Local Similarity 100.0%; Pred. No. 1.8e-68; Matches 140; Conservative 0; Mismatches 0; Indels C

Trownsend and rownsend knourie and Brancisco 11fornia 11f	RESULT 1 US-08-561-521-4  Sequence 4, Application US/08561521  Sequence 4, Application US/08561521  GENERAL INFORMATION:  APPLICANT: Leger, Olivier J.  APPLICANT: Sendana, Jose APPLICANT: Jones, S. Tarran  TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  TITLE OF INVENTION: Adhesion Molecule VLA-4  NUMBER OF SEQUENCES: 45	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	9 505.5 67.8 139 2 US-08-452-164A-8 Sequence 8, 504 67.6 254 2 US-08-792-824-4 Sequence 4, 504 67.6 254 2 US-08-792-824-7 Sequence 7, 504 67.6 254 2 US-08-792-824-7 Sequence 10, 504 67.6 254 2 US-08-792-824-10 Sequence 10, 504 67.6 254 2 US-08-646-265A-99 Sequence 13, 502 67.3 136 4 US-08-646-265A-99 Sequence 38, 500-56, 57.1 118 2 US-08-232-081B-38 Sequence 38, 500-56, 57.1 118 2 US-08-24, 57.1 118 2 U	ence 33, 6 m c 6 m	S-08-477-989B-96 S-08-477-989B-86 S-08-477-989B-86 S-08-477-989B-86 S-08-477-989B-86 S-08-477-989B-86 ALIGNMENTS ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  Steuart Tower, Suite s-Dos s-10, Version #1.25 '561,521 '186,269A '186,269A	cation US, 137 137 137 137 137 137 137 137 137 137	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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RESULT 4
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                                                           Gaps
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                                                                                                                                                                                                                                                                               APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            SEE: Townsend and Townsend Khourie and Crew :: One Market Plaza, Steuart Tower, Suite 2000 San Francisco California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 746; DB 5;
100.0%; Pred. No. 1.8e-68;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15270-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                   Sequence 4, Application PC/TUS9501219 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                         121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                             121 YGNYGVYAMDYWGQGTSVTV 140
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                                                                                                                                                                                                                                                                APPLICANT: Bendig, Mary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Smith, William L. REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 140 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein PCT US95-01219-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94105
                                                                                                                                                                                                                    PCT-US95-01219-4
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80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
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                                                                                                                                                                                           TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 86.5%; Score 645; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2.6e-58;
Matches 121; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/186,269A
                                                                                                                                                                                                                                                                                                                                                                                                                                          :: Floppy disk
IBM PC compatible
:YSTEM: PC-DOS/MS-DOS
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                                         Sequence 9, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFRENCE/DOCKET NUMBER: 1527
TELECOMMULICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                      APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Ollvier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
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APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 amino acids
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APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                     California
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RESULT 3
US-08-561-521-9
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ZIP: 20007-5109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DPRFQGRATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                       TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 123;
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US-08-646-265A-29
Sequence 29, Application US/08646265A
Sequence 29, Application US/08646265A
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
APPLICANT: STOC, Koh
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: RESULABED HUMAN ANTIBODY
TITLE OF INVENTION: RESULABED HUMAN ANTIBODY
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COLOR COLON & CATTMENT ON TO COLOR & LARGHER COL
                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 86.5%; Score 645; DB 5; L
Best Local Similarity 100.0%; Pred. No. 2.6e-58;
Matches 121; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
        Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US95-01219-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                  94105
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61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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APPLICANT: MAECHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOHYA, Yukinobu
APPLICANT: TOHYA, Yukinobu
APPLICANT: MISHIYAMI, Takeshi
TITLE OF INVENTION: ANTI-FELINE CALCIVIRUS RECOMBINANT
TITLE OF INVENTION: ANTI-FELINE RECOMBINANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 84.9%; Score 633; DB 4; Length 136; Best Local Similarity 89.3%; Pred. No. 4.9e-57; Matches 125; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-OVV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HAROLG C.
REGISTRATION NUMBER: 53,258
REFERENCE/DOCKET NUMBER: 53,258
REFERENCE/DOCKET NUMBER: 53,258
REFERENCE/DOCKET NUMBER: 53,254
FILING DATE: 19-OVV-1993
ATTORNEY/AGENT NUMBER: 53,254
RECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER
STREET: 1233 20th Street, N.W., Suite 300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 5785968
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IBM PC compatible
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 29:
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TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
21P: 20036-8218
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-646-265A-29
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ADDRESSEE: WEGNER, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington STATE: D.C.
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US-08-024-253-2
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61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INCORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
TAPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.6%; Score 593.5; DB 3; Length 182.9%; Pred. No. 5.1e-53;
Live 6; Mismatches 13; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
      PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEEAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDENNIES: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: DS-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 17, Application US/08561521
; Patent No. 5840299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Smith, William L. REGISTRATION NUMBER: 30,223 REFERENCE/DOCKET NUMBER: 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YGNYGVYAMDYWGQGTSVTV 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-836-561-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.8%; Score 595; DB 1; Length 136; 82.9%; Pred. No. 3.5e-53; tive 8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NOTE, ENGRANCED APPLICANT: NOTE, ENGRANCED APPLICANT: NAKAMURA, Kazuyasu APPLICANT: IIDA, Akihiro APPLICANT: ANAZANA, Hideharu APPLICANT: ANAZANA, Hideharu APPLICANT: TAKATSU, Kiyoshi TITLE OF INVENTION: Receptor Against Human Interleukin-5 TITLE OF SEQUENCES: 106 CORRESPONDENCE ADDRESS:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P-500-23744
TELECHONIONICATION INFORMATION:
TELEPHONE: (202) 887-0400
TELEFAX: (202) 835-0605
TELEFAX: 440706 WEGNEN
SEQUENCE CHARACTERISTICS:
                                                              APPLICATION NUMBER: US/08/024,253
FILING DATE: 19933301
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 79189/1992
FILING DATE: 28-FEB-1992
ATTORNEY AGENT INFORMATION:
NAME: CANTOR, Herbert I.
REGISTRATION NUMBER: 24,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: Pennie & Edmonds LLP
:: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/08836561 Patent No. 6018032 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AW-----LAYWGQGTLVTV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KOIKE, Masamichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 136 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 82.99
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-836-561-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-024-253-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Pred. No. 4.9e-52;
Best Local Similarity 77.1%; Pred. No. 4.9e
Matches 108; Conservative 15; Mismatches
                                                                                                                                                                          121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                            121 YGNYGVYAMDYWGQGTLVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Smith, William L. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                          US-08-561-521-44
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                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                            1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.3%; Score 584; DB 5; Length 142;
                                                                                                                                                           78.3%; Score 584; DB 2; Length 142; 77.1%; Pred. No. 4.9e-52; vative 15; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 15.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                      121 YGNYGVYAMDYWGQGTLVTV 140
                  TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
 : 415-543-9600
415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 142 amino acids TYPE: amino acid
                                                                 LENGTH: 142 amino acids
                                                                                                                                                                                            Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                              ; MOLECULE TYPE: protein US-08-561-521-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                               Best Local Similarity
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 TELEPHONE:
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                                                                                                                                                              Query Match
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                                                                                                                                           61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                   0; Gaps
                                              1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                      Sequence 44, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saidanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 75.3%; Score 562; DB 2; Length 125; Local Similarity 89.4%; Pred. No. 7e-50; nes 110; Conservative 2; Mismatches 9; Indels
17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .B: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
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 61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARGYYYYDSXVGYYAMDYWGQGTX 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                      Sequence 44, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 562; DB 5; Length 125;
Pred. No. 7e-50;
2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                           E: Townsend and Townsend Khourie and Crew
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Opery Match 75.3%; Score 562; UB
Best Local Similarity 89.4%; Pred. No. 7e-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15270-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 125 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Smith, William L. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415-543-5043
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-44
                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                94105
                                    138 VTV 140
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                                                                    121 VTV 123
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                                                                                                                             RESULT 11
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61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
Patent No. 6258529
GENERAL INFORMATION:
APPLICANT: Berdoz, Jose
APPLICANT: Kraehenbuhl, Jean Pierre
ITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US95-15716-8
Sequence 8, Application PC/TUS9515716
GENERAL INFORMATION:
APPLICANT: Berdoz. Jose
APPLICANT: Kraehenbuhl, Jean Pierre
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Indels
                                                                                                                                                                                                                                                                        COUNTY: USA
ZIP: 0110-2804
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.3%; Score 554; DB 4;
80.7%; Pred. No. 5.1e-49;
tive 6; Mismatches 15
                                                                                                                                                                                     ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Fish & Richardson
225 Franklin Street, Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 06132/009001
REFERENCE/DOCKET NUMBER: 06132/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 YGNYGVYAMDYWGQGTSVTV 140
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 136 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.78
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-348-548-8
                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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ZIP: 02110-2804
COMPUTER READABLE FORM:
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STREET: 44.
TTY: Boston
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application PC/TUS9501219 GENERAL INFORMATION:
                                                            NAME: Smith, William L.
REGISTATION UNDBER: 30,23
REFERENCE/DOCKET NUMBER: 1527
TELECOMMUNICATION INPORMATION:
TELEPHONE: 415-543-9600
TELEPAX: 415-543-9600
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                   FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                   123 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein US-08-561-521-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/08561521
Patent No. 584029
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.3%; Score 554; DB 5; Length 136; 80.7%; Pred. No. 5.1e-49; tive 6; Mismatches 15; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                APPLICATION NUMBER: US 08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/FAGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/009001
TELECOMMUNICATION INFORMATION:
TELEFAN: (617) 542-5070
                                                                                                          APPLICATION NUMBER: PCI/US95/15716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/561,521
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 YGT -- SYWFPYWGQGTLVTV 134
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                                                                                                                                                                                                                                                                                                                                                                                                                           136 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US95-15716-8
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California
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Best Local Similarity
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US-08-561-521-11
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Gaps
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APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha. Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
CORRESPONDENCE: 45
CORRESPONDENCE: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.9%; Score 544; DB 2; Length 123; Best Local Similarity 82.6%; Pred. No. 4.6e-48; Matches 100; Conservative 11; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
US/08/186,269A
APPLICATION NUMBER:
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0;
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                                                                                                             Query Match 72.9%; Score 544; DB 5; Length 123; Best Local Similarity 82.6%; Pred. No. 4.6e-48; Matches 100; Conservative 11; Mismatches 10; Indels
                                                                                                                                          10; Indels
                                                                                                                                                                                                                                                                                                                                               Search completed: January 6, 2003, 13:19:08
Job time : 12.596 secs
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-11
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January 6, 2003, 13:17:36; Search time 6.78788 Seconds (without alignments) 390.875 Million cell updates/sec
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746
1 MKCSWVMFFLMAVVTGVNSE.....YGNYGVYAMDYWGQGTSVTV 140
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14: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117078 seqs, 18951520 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                   - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                      OM protein
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Sequence 19, Appl		Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	⋖	Sequence 38, Appl	Sequence 18, Appl	Sequence 4, Appli	Sequence 7, Appli	Sequence 11, Appl	Sequence 23, Appl	Sequence 22, Appl	Sequence 29, Appl	Sequence 28, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 28, Appl
ΠD	US-09-910-059-19	US-09-564-329A-11	US-09-855-153-11	US-09-854-811-11	US-09-934-773-11	US-09-963-620-11	US-09-809-739-5	US-09-968-851-38	US-09-158-120A-18	US-09-861-294-4	US-10-032-482-7	US-09-910-059-11	US-09-976-787-23	US-09-865-198-22	US-09-976-787-29	US-09-865-198-28	US-09-976-787-7	US-09-865-198-7	US-09-976-787-28
DB	10	10	10	10	10	10	10	6	10	10	6	10	10	10	10	10	10	10	10
Query Match Length DB	255	136	136	136	136	136	139	535	117	153	112	120	117	117	238	238	117	117	240
Query Match	62.9	65.5	65.5	65.5	65.5	65.5	64.8	63.7	63.7	63.5	62.7	62.5	61.8	61.8	61.8	61.8	61.7	61.7	61.7
Score	491.5	488.5	488.5	488.5	488.5	488.5	483.5	475.5	475	473.5	467.5	466.5	461	461	461	461	460	460	460
Result No.	г	7	က	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19

20 460 61.7 240 10 US-09-865-19 45.5 61.3 138 10 US-09-78-95 44.2 59.1 140 10 US-09-78-78 24 44.7 59.9 139 12 US-10-006-79 25 44.2 59.2 136 9 US-09-956-206 26 44.2 59.2 136 9 US-09-956-206 27 44.0 5 59.0 124 9 US-09-974-052 28 44.0 5 59.0 124 9 US-09-974-052 28 44.0 5 59.0 124 9 US-09-974-052 29 44.0 5 59.0 124 9 US-09-914-052 29 44.0 5 59.0 124 9 US-09-991-98 24 42.0 5 50.0 124 9 US-09-91-052 29 44.0 5 59.0 124 9 US-09-91-052 20 44.0 5 59.0 124 9 US-09-91-052 20 44.0 5 50.0 124 9 US-09-91-052 21 42.1 5 56.1 17 10 US-09-91-18-19-19-19-19-19-19-19-19-19-19-19-19-19-
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16; Indels 11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 FFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REFERENCE: 30435.54USI4
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.5%; Score 488.5; DB 10; Length 136; 74.4%; Pred. No. 5.8e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Mismatches
                  TITLE REPERENCE: 30435.540514
CURRENT APPLICATION NUMBER: US/09/855,153
CURRENT FILING DATE: 2001-05-14
PRIOR PAPLICATION NUMBER: 09/564,329
PRIOR FILING DATE: 2000-05-03
PRIOR PILING DATE: 1999-07-20
PRIOR PILING DATE: 1999-07-20
PRIOR PILING DATE: 1999-07-10
PRIOR PILING DATE: 1998-01-12
PRIOR PELING DATE: 1998-01-12
PRIOR PELING DATE: 1998-01-12
PRIOR PELING DATE: 1998-02-13
PRIOR PELING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR PELING DATE: 1998-12-21
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CURRENT FILING DATE: 2010-05-14
PRIOR PPLICATION NUMBER: 09/564,329
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
NUMBER OF SEO ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR PAPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
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PRIOR APPLICATION NUMBER: 09/308,503
PRIOR FILING DATE: 1999-05-25
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Best Local Similarity 74.4%
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
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US-09-854-811-11
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LENGTH: 136
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;
                                                                                                                                                                                                                                                                                                         APPLICANT: Relter, Nobert E.
APPLICANT: Witte, Owen N.
TILE CF INVENTION: PSCAT: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.540S14
CURRENT APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1997-07-20
PRIOR APPLICATION NUMBER: 08/414,279
PRIOR FILING DATE: 1998-01-20
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
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                                                                                                                                                                         RESULT 2
2-09-564-329A-11
; Sequence 11, Application US/09564329A
; Patent No. US20010055751A1
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Patent No. US200201026681
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
                         124 YGVYAMDYWGQGTSVTV 140
                                                     121 AGYLAMDYWGQGTSVAV 137
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LENGTH: 136
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62 GWIDPENGDIEFVPKFQGKAIMTADIFSNIAYLHLSSLISEDTAVYYCKIGG----- 113
68 GRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reiter, Robert B.
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REPERENCE: 30435.54018.
CURRENT APPLICATION NUMBER: US/09/963,620
CURRENT FILING DATE: 2001-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION UNBER: 09/564, 329
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 1090-07-20
PRIOR PELING DATE: 1999-07-20
PRIOR PELING DATE: 1999-07-20
PRIOR PELING DATE: 1997-03-10
PRIOR FILING DATE: 1997-03-10
PRIOR PELING DATE: 1998-01-12
PRIOR PELING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-13
PRIOR PELING DATE: 1998-02-13
PRIOR PELING DATE: 1998-02-17
PRIOR PELING DATE: 1999-02-17
PRIOR PELING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-03-16
PRIOR PELING DATE: 1999-03-17
PRIOR APPLICATION NUMBER: 09/203, 939
PRIOR FILING DATE: 1999-02-17
PRIOR PELING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR PELING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR PELING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/09963620; Patent No. US20020141941A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 136
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114 ---FWGOGTLVTV 123
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JS-09-963-620-11
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US-09-963-620-11
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APPLICANT: WILLE, NODGET E.
APPLICANT: SAFFRAN, DOUGUBAS C.
TITLE OF INVENTION: PSCA PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.540514
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: 2000-05-03
PRIOR PLICATION NUMBER: 09/59,326
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-02-31
PRIOR FILING DATE: 1998-02-31
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1998-02-17
PRIOR FILING DATE: 1998-12-21
PRIOR FILING DATE: 1998-12-21
PRIOR FILING DATE: 1998-12-02
PRIOR FILING DATE: 1998-12-02
PRIOR FILING DATE: 1998-12-02
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR PRIOR PRILCATION NUMBER: 09/203,93
PRIOR FILING DATE: 1999-02-17
PRIOR PRIOR PRILCATION NUMBER: 09/203,93
PRIOR FILING DATE: 1999-02-17
PRIOR PRIOR PRILCATION NUMBER: 09/203,93
PRIOR FILING DATE: 1999-02-17
PRIOR PRIOR PRILCATION NUMBER: 09/203,93
PRIOR FILING DATE: 1999-02-17
PRIOR PRIOR PRILCATION NUMBER: 09/203,93
PRIOR PRIOR PRILCATION NUMBER: 09/203,93
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                                                                                                                                                                                            16; Indels 11; Gaps
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                                                                                                                                                                                                                                                        8 FFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWI 67
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                                                                                                                          ch 65.5%; Score 488.5; DB 10; Length 136; 1 Similarity 74.4%; Pred. No. 5.8e-32; 99; Conservative 7; Mismatches 16; Indels 11;
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Patent No. US20020136689A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 AMDYWGQGTSVTV 140
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114 ---FWGQGTLVTV 123
                                                                                                                             Query Match
Best Local Similarity
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                             ; ORGANISM: SCID Mice US-09-854-811-11
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Query Match 65.5%; Score 488.5; DB 10; Length 136; Best Local Similarity 74.4%; Pred. No. 5.8e-32; Matches 99; Conservative 7; Mismatches 16; Indels 11; Gaps
                                                                                            ; Sequence 5, Application US/09809739
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Patent No.

FEATURE:

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19 SEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTK 78
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Patent No. US2002101257A1
GENERAL INFORMATION:
APPLICART: JOHNSON, L.
TITLE OF INVENTION: Respiratory Syncytical Virus
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, ADDRESSEE: STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.7%; Score 475.5; DB 9;
77.0%; Pred. No. 2.2e-30;
tive 11; Mismatches 10;
                                                                                                                       NAME: Strauss, William L.
REGISTRATION NUMBER: 47,114
REFERENCE/DOCKET NUMBER: 03804.0142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
INFORMATION FOR SEQ 1D NO: 38:
         APPLICATION NUMBER: PCT/FR96/01111
                                 FILLING DATE: 17-JUL-1996
APPLICATION NUMBER: FR 95/08729
FILING DATE: 19-JUL-1995
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469201-367
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September 21, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,592
FILING DATE: August 15, 1994
APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
                                                                                                  ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: Windows95
SOFTWARE: MS WOACH 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24,025
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 77.08
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: ROSELAND
STATE: NEW JERSEY
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US-09-158-120A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 38, Application US/09968851
Publication No. US20020193561A1
GENERAL INFORMATION:
APPLICANT: CONSELLLER, EMMANUEL
BRACCO, LAURENT
TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 64.8%; Score 483.5; DB 10; Length 139; Best Local Similarity 66.7%; Pred. No. 1.5e-31; Matches 94; Conservative 16; Mismatches 26; Indels 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,851
FILING DATE: 03-OCt-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION: <UNKnown>
APPLICATION: <UNKnown>
FILING DATE: 20-Peb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                CATION: (1)...(139)
CTHER INFORMATION: YFC51.1 heavy chain variable region
NAME/KRY: SIGNAL
LOCATION: (1)...(19)
CATION: (1)...(19)
US-09-809-739-5
              GENERAL INFORMATION:
APPLICANT: Horvath, Christopher J.
APPLICANT: Rao, Patricia E.
TITLE OF INVENTION: Method of Inhibiting Stenosis and
TITLE OF INVENTION: Restenosis
FILE REFERENCE: 1855.1069-003
CURRENT APPLICATION NUMBER: 02/09/809,739
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: US 09/528,267
                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 139
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US20020106369A1
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                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
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APPLICANT: Copley, Clive G
APPLICANT: Copley, Clive G
APPLICANT: Copley, Clive G
APPLICANT: Edge, Michael Derek
APPLICANT: Emery. Stephen Charles
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
TITLE OF INVENTION: Their Therapeutic use in an Adept System
FILE REPERENCE: 1991-209
CURRENT APPLICATION NUMBER: US 09/171,945
PRIOR APPLICATION NUMBER: US 09/171,945
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1997-04-29
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1996-05-04
SPRIOR FILING DATE: 1996-05-04
SPRIOR FILING DATE: 1996-05-04
SPRIOR FILING DATE: 1996-05-04
SPRIOR FILING DATE: 1996-05-04
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 131
SEQ ID NOS: 131
                                                                                                                                    APPLICANT: RUIZ, PEGRO
APPLICANT: EREZ-ALON, Neta
APPLICANT: EREZ-ALON, Neta
APPLICANT: EREZ-ALON, Neta
APPLICANT: HERKEL, Johannes
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR
TITLE OF INVENTION: IMMUNITY
FILE REFERENCE: COHEN42
CURRENT APPLICATION NUMBER: US/10/032,482
CURRENT PILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: PCT/IL98/00266
PRIOR APPLICATION NUMBER: PCT/IL98/00266
PRIOR APPLICATION NUMBER: IL 121041
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: IL 121041
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 LQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.5%; Score 466.5; DB 10; Length 120; 77.7%; Pred. No. 2.7e-30; Live 7; Mismatches 17; Indels 3;
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; Patent No. US20020142359A1
; GENERAL INFORMATION:
Sequence 7, Application US/10032482 Publication No. US20020197270A1 GENERAL INFORMATION:
                                                                                                                       Wolkowicz, Roland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92; Conservative
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Matches 94; Conservative
                                                                   APPLICANT: Cohen, Irun
APPLICANT: ROTTER, Varda
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                                                                                                                                                                                                                                               Length 117;
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; Sequence 4, Application US/09861294
; Sequence 4. Application US/09861294
; GEMERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOOM
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT PILING DATE: 2001-05-17
; PRIOR FILING DATE: 1998-06-11
; PRIOR FILING DATE: 1998-06-11
                                                                                                                                                                                                                                                                                            12; Indels
                                                                                                                                                                                                                                             63.7%; Score 475; DB 10; 76.9%; Pred. No. 5.7e-31; tive 10; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 38 SOFTWARE: FastSEQ for Windows Version 4.0
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                                               INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 AMINO ACIDS
TYPE: AMINO ACID
    TELEPHONE: 973-994-1700
TELEFAX: 973-994-1744
                                                                                                                                                                                                                                                                 Best Local Similarity 76.9%
Matches 93; Conservative
                                                                                                                                           TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN
US-09-158-120A-18
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; LOCATION: (1)...(19)
US-09-861-294-4
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LENGTH: 153
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Batent No. US20020064528A1

GENERAL INFORMATION:

APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REPERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT FILING DATE: 2000-11-12
PRIOR FILING DATE: 2000-01-28
                                      61.8%; Score 461; DB 10; Length 117; llarity 76.0%; Pred. No. 7.1e-30; Conservative 9; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Mindows
SEQ ID NO 29
LENGTH: 238
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Best Local Similarity 76.09
Matches 92; Conservative
                                      Query Match
Best Local Similarity
Matches 92; Conserv
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US-09-976-787-29
US-09-865-198-22
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Patent No. US20020103345al
APPLICAMT: Zhu, Zhenping
TITLE OF INVENTION: Production
FILE REPERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR PILING DATE: 2000-05-24
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                                                                                  80 DPKFQGKATITADISSNTAYLQLSSLTSEDIAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                     Gaps
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         20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY
                                                                                                                                                                                                                                                                               Squence 23, Application US/09976787

Squence 23, Application US/09976787

Patent No. US20020064528A1

GENERAL INFORMATION:

APPLICANT: Zhu, Zhenping

TITLE OF INFORMATION:

FILE REFERENCE: 11245,46505

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 60/117,726

PRIOR PILLING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 40

SOFTHARE: WordPerfect 8:0 for Windows
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Mouse
US-09-976-787-23
                                                                                                                                                                                                                                                                     US-09-976-787-23
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LENGTH: 117
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us-09-155-739-4.rpr

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: January 6, 2003, 13:12:26; Search time 13.0101 Seconds

(without alignments)
1034.490 Million cell updates/sec

Ferrect score: 740
Sequence: 1 MKCSWVMFFLMAVVTGVNSE......YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62 Gapext 0.5 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 2832

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum bs seq tength: Zuuuuuuuu Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: PIR\_7

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Oue:	.5 80.9 97 80.0	.5 76.5 137	5 76.1 123 2	72.3 120	5 69.9 122 2	15 69.0 115 2	67.0 116 2	98 66.8 120 2	.5 66.3 268 2	.5 66.2 108 2	92 66.0 221 2	5 63.3 114 4	63.1 140	5 62.5 139 2	5 62.3 139 1	.5 62.0 99 2	.5 61.9 115 2	.5 61.9 139 2	.5 61.7 141 2	59 61.5 135 2	59 61.5 140 1	.5 61.3 107 2	57 61.3 138 2	56 61.1 249 2
Query Match 80.9	80.0 80.0	76.5	76.1	72.3	6.69	0.69	67.0	9.99	66.3	66.2	0.99	63.3			62.3	62.0	61.9	61.9	61.7	61.5	61.5	61.3	61.3	61.1
Result No. Score	603.5 597	570.5	567.5	539	521.5		9 500		49	4		47	5 471	46	64.	462.	461.	461	460	4	4	457	4	456

19 heavy chain precursor V region (WRL-histone 7H) - mouse (fragment)
19 heavy chain precursor V region (WRL-histone 7H) - mouse (fragment)
2 Species: Mus musculus (house mouse)
2 Species: Mus musculus (house mouse)
2 Species: Was musculus (house mouse)
3 C; Date: 04-De 20 # sequence\_revision 04-Dec-1992 #text\_change 21-Jan-2000
3 Accession: 804576
8 KKfler, R.: Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.;
8 Eur. J. Immunol. 17, 91-95, 1987
8 KKfler analysis of the murine lupus-associated anti-self response: involv A; Reference number: 804573; MUID:87133856; PMID:310255
8 A; Recession: 804573; MUID:87133856; PMID:310255
8 A; Residues: 1-136 <ARPS
A; Residues: 1-136 <ARPS
A; Cross-references: EMBL:X14624; NID:952029; PIDN:CAA32777.1; PID:952030
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 1-19/Domain: signal sequence #status predicted <AMAT>
F; 20-136/Product: Ig heavy chain V region (fragment) #status predicted <AMAT>
F; 34-117/Domain: immunoglobulin homology <IMM>

Ig heavy chain pre	Ig heavy chain V r	Ig gamma-2a chain	Ig heavy chain V r	Ig gamma chain - m	Ig gamma-2a chain	Ig heavy chain V r	Ig heavy chain V r								
PC1155	S25174	S21810	PH1484	PH1493	S37483	PH1494	PH1489	PH1486	PH1488	S41394	S20643	838950	S40295	S20646	C37262
~	~	~	7	7	7	~	7	2	~	~	~	a	~	~	~
	•									•	•		•	•	
133	118	138	140	135	469	135	140	140	140	120	122	246	446	123	66
60.9 133		•	. ,		•		•					•	•		
• •	6.09	6.09	. 2.09	9.09	60.5	60.5	. 6.65	59.5	59.1	29.0	29.0	59.0	29.0	58.8	58.7

## ALIGNMENTS

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ñ
                                    Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S29594
R;Seymour, R.
submitted to the EMBL Data Library, February 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IGRIDPANGYTEYDPKFQGKATITADTSTNTAYLQLSSLTSEDTAVYYCTG----GNY-A 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 IGRIDPANGYIKYDPKFQGKATITADISSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGV 126
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IFFLMAVVIGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDIYMHWVKQRPKQGLEM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                   7 MFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEW 66
                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                            80.9%; Score 603.5; DB 2; Length 178; 88.1%; Pred. No. 2.1e-45; ive 6; Mismatches 5; Indels 5
                                                                                                                                                                                                                                                                                                                                                                     88.1%;
                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 88.1
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 YAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: S29593
                                                                                                                                                                                                               A;Status: preliminary
.. A;Molecule type: mRNA
A;Residues: 1-178 <SEY>
                                                                                                                                                                                                                                                                                                                                                 Query Match
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RESULT 1
                      S29594
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A. Molecule type: mRNA
A. Residues: 7-120 <RCO1>
A. Residues: 7-120 <RCO1>
A. Residues: 7-120 <RCO1>
A. Residues: 7-120 <RCO1>
A. References: EMBL:X01820; NID:951833; PIDN:CAA25962.1; PID:91333983
A. Note: this sequence was determined from the differentiated gene
B. Rocca-Serra, J.; Mazie, J.C.; Moinler, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
J. Immunol. 129, 2554-2559, 1982
A. Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not
A. Reference number: 807453; MUID:83058021; PMID:6815271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     If heavy chain V region (EB) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 22-Mov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S1789
B;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A;Title: Biochemical implications from the variable gene sequences of an anti-cytochr
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gradus Chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S03471; S07453
B;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKCSWVMFF1MAVVT-GVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQR 59
                                                                                                                                                                                                             4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                  60 PEQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCA 116
                                                                                                                                                                                                                                                                                                                61 PEQGLEWIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCA 117
                                                                                                                                         1;
                                                                                     Length 123;
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A/Molecule type: protein
A/Recidues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 539; DB 2; Length 120;
Pred. No. 5.6e-40;
...artches 7; Indels
                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S03471; MUID:84057768; PMID:6416834
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                                                                                  DB 2;
                                                                                                     Pred. No. 1.9e-42;
3; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                    76.1%; Score 567.5;
94.9%; Pred. No. 1.9
                        F;35-118/Domain: immunoglobulin homology <IMM>
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.3%;
89.3%;
                                                                                                                        Matches 111; Conservative
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                                                                          Query Match
Best Local Similarity
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A; Status: preliminary
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R; Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A; Description: Specific amplification by the polymerase chain reaction of rearranged gen A; Reference number: $52445
A; Accession: $52445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: PH1403
R; Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta
J. Exp. Med. 176, 1209-1214, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in
                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region (clone micro m- 46-6, 46-12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                    61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: X82690; NID: 9673439; PIDN: CAA58011.1; PID: 9673440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 BQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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                                                                                                                                                 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                     Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin V region; immunoglobulin homology
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                       12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Indels
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                   Score 597; DB 2;
Pred. No. 5.9e-45;
6; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 81.4%; Pred. No. 1.2e-42;
Matches 114; Conservative 6; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Superfamily: immunoglobulin V region; immunog
C;Keywords: heterotetramer; immunoglobulin
F;34-115/Domain; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                              121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                            117 --TYGAYAMDYWGQGTSVTV 134
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             Query Match 80.0%;
Best Local Similarity 82.9%;
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-137 <BER>
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A; Residues: 1-123 <SHI>
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A; Note: this sequence was determined from the differentiated gene R; Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug J. Immunol. 129, 2554-2558, 1982
A; Immunol. 129, 2554-2558, the mouse gamma-chains anti-GAT repertoire does not A; Reference number: S07453; MUID:83058021; PMID:6815271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, September 1991
A; Description: Cloning and sequencing of the CDNA coding for the variable regions of
A; Reference number: S24287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S24289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARWAGYY------FDYWGQGTTLT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Cross-references: EMBL:X62705; NID:951690; PIDN:CAA44584.1; PID:91333963 C.Superfamily: immunoglobulin V region; immunoglobulin homology C.Keywords: immunoglobulin P:14-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR-EGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DPKFQGKATITTDTSSNTAYLQFSSLTSEDTAVYYCARGTTVGR-----DYWGQGTTLT 114
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVOLOOSGAELVKPGASVKLSCTASGFNIKDTYIHCVKORPEOGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 VQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment) C;Species: Mus musculus (house mouse) A;Variety: strain BALB/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 1-43 <R802.>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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81.0%; Pred. No. 1.3e-36;
                                                                                                                                                                                                                                                                                                                                                                     Score 515; DB 2;
Pred. No. 6.6e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     69.0%;
83.5%;
A; Molecule type: mRNA
A; Residues: 10-115 <ROC1>
A; Cross-references: EMBL:X03219
                                                                                                                                                                                                                                                                                                                                                                                                                     tches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98; Conservative
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-116 <MON>
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                                                                                                                                                                                                   A; Accession: S07453
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S24289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M. EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAJ
                                                                                                                                                                                                                       3;
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C;Species: Mus musculus (house mouse)
A;Variety: strain BALBA/C
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03482; S07453
                                                                                                                                                                                                                                                                                                                                                                     79 YDPKFQGKATITADISSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSV 138
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                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                       20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                A;Cross-references: EMEL:X60683; NID:951820; PIDN:CAA43095.1; PID:951821
C;Superfaaily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterottetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                         Length 117;
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A; Accession: $03482
A; Status: preliminary
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ilarity 86.9%; Pred. No. 1.9e-38;
Conservative 4; Mismatches 9;
                                                                                                                                                                    10.1%; Score 523; DB 2; ilarity 85.2%; Pred. No. 1.4e-38; Conservative 7; Mismatches 3
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A; Residues: 1-122 <MIL>
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                                                                                                                                                                                                   Similarity
  A; Molecule type: mRNA
A; Residues: 1-117 <MYL>
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114 TV 115
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Matches 104;
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Matches
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Iggamma-1 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar 1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C;Accession: S49220
R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
Submitted to the EMBL Data Library, September 1994
A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing A;Reference number: S49220
                                                                                                                                                                                                                                                                                         RTILIDAR, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A.Tiller Both IgM and IgG anti-DNA antibodies are the products of clonally selective A.Feference number: PH0971; MUID:92381444; PMID:1512540
A.Saccession: PH1012
A.Saccession: P
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                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1012
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A/Residues: 1-221 <KIP>
A/Residues: 1-221 <KIP>
A/Residues: 1-221 <KIP>
A/Residues: nemal: 237502; NID:g541778; PIDN:CAA65732.1; PID:g541779
A/Residues: scrain Balb/c
G/Superfamily: immunoglobulin C region; immunoglobulin homology
E/1-120/Domain: V region #status predicted <VRG>
F/121-221/Domain: C region #status predicted <CRG>
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                                                                                                                                                         Ig heavy chain V region (clone 17p.73) - mouse (fragment)
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                            A.Note: this sequence was determined from the differentiated gene R.Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere J. immunol. 129, 2554-2558, 198.
A.Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se A.Reference number: S07453; MUID:83058021; PMID:6815271
                                                                                                                                              A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT
hypervariable regions.
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C'Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C'Adcession: A56446
R'Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
Biol. Chem. 270, 7829-7885; 1995
A'Title: A high affinity digoxin-binding protein displayed on MI3 is functionally idential Reference number: A56446; MUID:95229583; PMID:7713873
                                                           R:Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.
EMBG J. 2, 867-872, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ï
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000 C;Accession: S03484; S07453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 YDPKFQGKATITADISSNTAYLQLSSLTSEDIAVYFCAREGYYGNYGVYAMDYWGQGTSV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AQVKLQESGABLVKPGASVKLSCTTSGFNIKDTYMHWVKQRPEQGLEWIGRIAPANGITK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 SEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.8%; Score 498; DB 2; Length 120; 82.6%; Pred. No. 2.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 1-43 <ROC2>
C; Süperfamily: immunoglobulin V region; immunoglobulin homology
F; 15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
                                                                                                                                                                                                                     A; Reference number: S03471; MUID: 84057768; PMID: 6416834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 494.5; DB 2
Pred. No. 9.5e-36;
8; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Mdlecule type: mRNĀ
A;Residues: 1-268 <TAN>
A;Cross-references: GB:(120617
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.3%;
                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 10-120 <ROC1>
A; Cross-references: EMBL:X07144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity oz.u.
Matches 100; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                     A; Status: preliminary
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                                                                                                                                                                                                                                                       A; Accession: S03484
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R;Glusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that hav
                                                                                                                                       Ricesley, S.A.; Patten, P.A.; Schultz, P.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 1160-1165, 1993
Affittle: A genetic approach to the generation of antibodies with enhanced catalytic acti
A;Reference number: A47271; MUID:93165660; PMID:8094556
A;Accession: A47271
nitrophenyl phosphonate-specific antibody 48G7 heavy chain VDJ - synthetic (fragment)
                             C.Species: synthetic
A.Note: Mus musculus (house mouse) gene engineered and expressed in Escherichia coli
C.Date: 21-Sep-1993 #sequence_revision 11-Aug-1995 #text_change 11-Aug-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 DPKFQGKATITADISSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                            A; Molecule type: DNA; protein
A; Residues: 1-114 <LES>
A; Note: sequence extracted from NCBI backbone (NCBIN:124854, NCBIP:124855)
A; Note: parts of this sequence were determined by protein sequencing
F;22-96/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 16/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F; 34-117, Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: PH1482; MUID:93171820; PMID:8436910
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 472.5; DB 4;
Pred. No. 3.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-140 <GIU>
A; Experimental source: hybridoma cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.3%;
Best Local Similarity 77.7%;
Matches 94; Conservative
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                                                                                                                   C; Accession: A47271
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Search completed: January 6, 2003, 13:18:19 Job time: 14.0101 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 6, 2003, 12:48:25; Search time 7.07071 Seconds (without alignments) 821.231 Million cell updates/sec Run on:

US-09-155-739-4
746
1 MKCSWVMFFLMAVVTGVNSE.....YGNYGVYAMDYWGQGTSVTV 140 Title:
Perfect score: 7
Sequence: 1

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 Total number of hits satisfying chosen parameters:

112892 seqs, 41476328 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		æ			SUMMAKIES	
Result No.	Score	Query	Length	DB	ID	Description
-		600	0.51	-	TOTAL POINT	
- (	•	2.50	1.09	٠,	HVO/_MOUSE	
7	۵. ا	C.10	140	٠,	HVUZ_MOUSE	mus
3	425	7	120	Н	HV03_MOUSE	mns
4	422.5	ė.	137	Н	HV11_MOUSE	P01755 mus musculu
S	416	55.8	138	П	HV48_MOUSE	P03980 mus musculu
9	411	55.1	117	Н	HV09_MOUSE	P01753 mus musculu
7	396	53.1	136	Н	HV15_MOUSE	PO1759 mus musculu
<b>σ</b> ο	393	52.7		-	HV06_MOUSE	P01750 mus musculu
6	393	52.7		7	HV49_MOUSE	snu
10	389	52.1		-	HV10_MOUSE	P01754 mus musculu
11	388	52.0		ч	HV04_MOUSE	P01748 mus musculu
12	381	51.1		7	HV52_MOUSE	snu
13	379	50.8	117	П	HV13_MOUSE	P01757 mus musculu
14	379	50.8		П	HV01_MOUSE	P01745 mus musculu
15	378.5	50.7		П	HV1C_HUMAN	P01744 homo sapien
16	374	50.1		-	HV05_MOUSE	mus m
17	374	50.1		П	HV12_MOUSE	P01756 mus musculu
18	372	49.9		П	HV14_MOUSE	P01758 mus musculu
19	368.5	49.4		П	HV51_MOUSE	mus m
20	367	49.2		-	HV1B_HUMAN	P01743 homo sapien
21	360.5	48.3		-	HV50_MOUSE	mus m
22	359	48.1		П	HV1G_HUMAN	P23083 homo sapien
23	356.5	47.8		-	HV16_MOUSE	P01783 mus musculu
24	321.5	43.1		<del></del> 1	HV00_MOUSE	P01741 mus musculu
25	316.5	42.4	119	Н	HV38_MOUSE	P01808 mus musculu
56	315	42.2		Н	HV42_MOUSE	P01812 mus musculu
27	314	42.1		-	HV1A_HUMAN	P01742 homo sapien
28	312.5	41.9	119	Н	HV37_MOUSE	_
29	311	41.7		-	HV01_RAT	P01805 rattus norv
30	310.5	41.6		-	HV40_MOUSE	_
31	304	40.8			HV39_MOUSE	mus
32	297	σ,	137	-	HV46_MOUSE	22 mus
33	787	39.8	144	-	HV26_MOUSE	PO1795 mus musculu

P80421 homo sapien											P06326 homo sapien
HV1H_HUMAN	HV41_MOUSE	HV05_CARAU	HV36_MOUSE	HV24_MOUSE	HV3C_HUMAN	HV3T_HUMAN	HV3G_HUMAN	HV43_MOUSE	HV2I_HUMAN	HV3A_HUMAN	HV1F_HUMAN
1	П	Н	П	Н	-	Н	Н	H	Н	Н	-
120	117	116	116	123	117	116	122	144	146	122	125
39.3	39.1	39.1	38.9	38.9	38.6	38.3	38.1	38.1	38.1	37.9	37.8
293.5	292	291.5	290	290	288	285.5	284.5	284	284	282.5	282
34	32	36	37	38	39	40	41	42	43	44	45
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Query Match
                        RESULT 3
HV03_MOUSE
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                                                                              EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
                                  Gaps
                      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; PO1810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
SMART; SM00407; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                   MEDLINE-82152818; Pubmed-6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
Capra J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.5%; Score 459; DB 1; Length 140; 63.6%; Pred. No. 2e-37; ...tve 18; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                  "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG HEAVY CHAIN V REGION 9367.
 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
  Mismatches
                                                                                                                                                                                                                                              Ig heavy chain V region 93G7 precursor.
 18;
                                                                                                             121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                           121 YGS---SYFDYWGQGTTLIV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YG--GSYDFDYWGQGTPLTV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J00493; AAA38128.1; -. PIR; A02028; HVMSG7.
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
91;
                                                                                                                                                                                        HV02_MOUSE
P01746;
                                                                                                                                                                                                                                                                                                                           STRAIN=A/J;
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SEQUENCE
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Matches
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"The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";

Eur. J. Immunol. 12:1023-1032(1982).

-I MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER

DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS

CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibodies: somatic mutation evident in a gamma 2a variable region.";
Cell 24:625-637(1981).
-!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 VQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostom1;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; 1g; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-88131846; PubMed-6186498;
Siekevitz M., Gerem M.L., Brodeur P., Riblet R.,
Marshavitchin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.0%; Score 425; DB 1;
68.3%; Pred. No. 3.1e-34;
ilve 14; Mismatches 22;
                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
   120 AA.
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   PRT;
                                                                                                                                                Ig heavy chain V region 36-65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P01789; IMCP,
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 68.3% les 82; Conservative
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEGMENT, JH2.
PIR; A02028; HVMSG7.
                                                                                                                                                                      Mus musculus (Mouse)
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P01755;
HV03 MOUSE
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us-09-155-739-4.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-64248078; PubMed-6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Illegitimate recombination generates a class switch from C mu to C delta in an IgD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
PIR; A02033; HVMST7.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 137;
                                                                                                                                                                                                                                                                   COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                                                                                                                 COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                           56.6%; Score 422.5; DB 1; Length 61.4%; Pred. No. 6.3e-34; ive 16; Mismatches 33; Indels
                                                                                                                                                                                                                                         IG HEAVY CHAIN V REGION S43
                                                                                                                                                                                                                                                                                                                                                                                15200 MW; ADD5881BF44B8EC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region TEPC 1017 precursor. Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
                                                                                                                                                                                                                                                                                                            FRAMEWORK-3.
D SEGMENT.
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                                                                                                                                                                                                                                                                                   FRAMEWORK - 2
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                                                                                                                                                                                                              Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 LGRY----FDYWGQGTTLTV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                           EMBL; J00539; AAA38172.1; -. PIR; A02038; GJMS43. HSSP; P01810; 2FBJ. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                         61.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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SMART; SM00406; IGv; 1.
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54
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117
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SMART; SM00406; IGv; 1
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137 1
137 AA;
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P03980;
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Immunoglobulin V region; Signal

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Baltimore D.;
"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).

-I MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                        61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR-EG 119
                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                .
9
             HEAVY CHAIN V REGION TEPC 1017.
                                                                                                                                                                    ; Score 416; DB 1; Length 138;
; Pred. No. 2.7e-33;
21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 411; DB 1; Length 117;
Pred. No. 6.7e-33;
                                    COMPLEMENTARITY - DETERMINING - 1,
                                                               COMPLEMENTARITY - DETERMINING - 2.
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                                                                                        COMPLEMENTARITY - DETERMINING - 3.
                                                                                                                                                                                             29; Indels
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54 COMPLEMENTARITY-DETERMINING-
68 COMPLEMENTARITY-DETERMINING-
117 FRAMEWORK-3.
115 BY SIMILARITY.
117
11890 MW; 16191A088CB17F5A CRC64;
                                                                                                                                           15576 MW; 748157E4C6907B8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   HV09_MOUSE STANDARD; PRT; 117 AA. P01753; P11271; Created)
01-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                                                   BY SIMILARITY.
                                                   FRAMEWORK - 2
            IG HEAVY CH
FRAMEWORK-1
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                                                                             FRAMEWORK-3
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                                                                                                                                                                                                                                                                                                                                                121 YYDWF-----VYWGQGTLVT 135
                                                                                                                                                                                                                                                                                                                             120 YYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                  55.8%;
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68.4%;
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HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                             84; Conservative
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SMART; SM00406; IGv; 1.
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117 AA;
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                                                                                                                                           138 AA;
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                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-8222262; PubMed-6806821;
KRAPP M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
Blatther F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                           1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                 "Simultaneous expression of immunoglobulin mu and delta heavy chains by a cloned B-cell lymphoma: a single copy of the VH gene is shared by two adjacent CH genes.";

Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
                                                    1 MGWSCIMLFLAATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLOLSSLTSEDTAVYFCAR 117
                                                                                           61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDTSSSTAYMQLHSLTSEDSAVYYCAR 117
                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Indels
 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;
                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Mismatches
                                                                                                                                                                                                                                             Ig heavy chain V region BCL1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; 1g; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region; Signal.
                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 YGNY----FDYWGQGTTLTV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J00494; AAA38130.1; -. PIR; AAQ42; HVMSB1. HSSP, P01772; 2F84. InterPro; IPR0033006; Ig_MHC. InterPro; IPR003596; Ig_V.
 Conservative
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                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                  NCBL_TaxID=10090;
80;
                                                                                                                                                                        HV15_MOUSE
P01759;
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SEQUENCE
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HV06\_MOUSE

RESULT 8

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                                                                                                                                                                                                                                                                                                                                                     "Heavy chain variable region contribution to the NPb family of antibodies: sometic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).

-I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES. PIR, A02032; THOMSO2.

HSSP; P01810; 2FBJ.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-85099340; PubMed-2578321;
Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression of unrearranged VH genee segments.";
Cell 40:271-281(1985).
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Dest Local Similarity 65.5%; Pred. No. 3.6e-31;

Best Local Similarity 65.5%; Pred. No. 3.6e-31;

Matches 76; Conservative 17; Mismatches 23; Indels

Matches 76; Conservative 17; Mismatches 23; Indels
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IIG heavy chain V region VH558 B4 precursor.
Mus musculus (Mouse).
                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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    117 AA
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                                                                                                         Ig heavy chain V region 102 precursor.
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SMART, SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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InterPro; IPR003596; Ig_V.
  STANDARD;
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                                                                                                                                       Mus musculus (Mouse).
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117 1
117 AA;
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                                                                                                                                                                                                                                                                     STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                    Baltimore D.;
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P06328;
HV06_MOUSE
P01750;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                           "Heavy chain variable region contribution to the NPD family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-67(1981).
-i- MISCELLANEOUS: THIS GENALINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.7%; Score 393; DB 1; Length 117; 65.8%; Pred. No. 3.6e-31; ive 14; Mismatches 26; Indels
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                                                                                                                                            or send an email to license@isb-sib.ch).
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HSSP; POIGH10; ZFBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
Ffam; PR00047; ig; 1.
Immunoglobulin V region; Signal.
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"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).
-!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                               52.1%; Score 389; DB 1; Length 117; 65.8%; Pred. No. 8.8e-31; Live 15; Mismatches 25; Indels
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                                                                                                                               COMPLEMENTARITY - DETERMINING-1.
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                                                                                                    IG HEAVY CHAIN V REGION 145.
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11arity 64.1%; Pred. No. 1.1e-30;
Conservative 15; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
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21-JUL-1986 (Rel. 01, Last sequence up
21-JUL-1999 (Rel. 38, Last annotation
1g heavy chain V region 23 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A02030; HVMS23.
HSSP; PO1810; ZFBJ.
InterPrc; IPR003006; Ig_MHC.
InterPrc; IPR003596; Ig_V.
Pfam; PR00407; ig; 1.
SMART: SMO0406; IGv; 1.
Immunoglobulin V region; Signal.
HSSP; P01810; 2FBJ.
interPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL.
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                                                                                                                                                                                                                                                             77; Conservative
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54
68
85
117
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Best Local Similarity
75; Conserve
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                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    HV04_MOUSE
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SEQUENCE
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HV04_MOUSE
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region J558.
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P01745;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
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                  1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
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                                                   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
                                                                 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-Aurany Chain V region VH558 Al/A4 precursor.
Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG HEAVY CHAIN V REGION VH558 A1/A4.
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MEDLINE-85099340; PubMed-2578321;
Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.1%; Score 381; DB 1; Length 117; 65.5%; Pred. No. 5.2e-30; ive 16; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                        117 AA.
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                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                    unrearranged VH gene segments.";
Cell 40:271-281(1985).
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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                                                                                                                                    HV52_MOUSE
P06327;
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NON_TER
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117 AA.

PRT;

STANDARD;

RESULT 13 HV13\_MOUSE ID HV13\_MOUSE

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Zakut R., Cohen J., Givol D.;
Nucleic Acids Res. 8.4839-4840(1980).
-!- MISCELIANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A WYELOWA THAT SECRETES IGG2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the CDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
pheavy chain V region MPC 11.
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InterPro; IPR003596; Ig_W.
Pfam, PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin_V region.
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HSSP; P01789; 1MCP.
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                                                       NCBI_TaxID=10090;
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Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
(In) Bach M.K. (eds.);
Immediate hypersensitivity: modern concepts and developments, pp.1-36,
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                                                                                                                                                                                                                                                                                                                                                                                                                     20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
LoCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 heavy chain V-I region ND precursor (Fragments).
Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-i- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
                                                                                                                                                                                                                                                                                                50.8%; Score 379; DB 1; Length 121; 62.0%; Pred. No. 8.4e-30; Live 17; Mismatches 27; Indels
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                                                                                                                                                                                                                                            SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
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IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
PIR; A02027; GVMS11.
HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Matches 75; Conservative
                                                                                                           Pfan, PF00047; ig; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region. NON_TER 121 121
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P01744;
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DISULFID
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SEQUENCE
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ID HY1C_HIM

ID HY1C_HIM

ID 11-0CT

ID 11-
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16491 MW; 948F9F72A5366C20 CRC64;

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                                                              9 FLMAVVIGVNSEVQLQQSGAELVKPCASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIG 68
                                                                              50.7%; Score 378.5; DB 1; Length 147; 52.6%; Pred. No. 1.2e-29; ive 25; Mismatches 35; Indels 5;
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Job time: 8.07071 secs
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129 DYSYTLDVWGQGTTVTV 145
                                Conservative
                 Best Local Similarity
Matches 72; Conserv
   Query Match
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746
1 MKCSWVMFFLMAVVTGVNSE......YGNYGVYAMDYWGQGTSVTV 140
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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3: sp_fungi:*
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5: sp_invertebrate:*
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7: sp_mhc:*
8: sp_cyganelle:*
9: sp_phage:*
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sp_virus:*
sp_vertebrate:*
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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tion	Snu	шns	mns	snw	mus	snw	mus	шns	mns	snw	mus	mns	mus	шns	Bus	mus
Description	099131	099125	091185	09d814	Q8vcx7	Q924q3	Q8vcx4	08vdc9	Q924r4	Q924r1	Q91wt1	Q91wr1	0924d6	0991c4	Q91wt3	Q924q1
ΔΙ	Q99L31	Q99L25	Q9JL85	Q9D8L4	Q8VCX7	092403	Q8VCX4	Q8VDC9	Q924R4	Q924R1	Q91WT1	Q91WR1	092406	Q99LC4	Q91WT3	992401
	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11
Query Match Length DB	468	473	109	473	613	146	489	168	145	145	481	488	145	463	481	142
Query Match	79.0	66.3	64.3	64.1	0.09	59.4	58.8	58.6	57.8	57.8	57.5	57.2	57.0	57.0	57.0	56.8
Score	589	494.5	480	478	447.5	443	439	437	431.5	431.5	429	426.5	425.5	425.5	425	424
Result No.	-	7	٣	4	5	9	7	8	6	10	11	12	13	14	15	16

	0924F8 mus musculu 0924F5 mus musculu 09z1c4 mus musculu 09qxf0 mus musculu 09j177 mus musculu 09d9b8 mus musculu
0924 RB 0924 RD 0924 RD 0924 RD 0924 RD 0924 RD 0924 RD 0924 RT 0924 RB 0924 RB	0924P8 0924R5 0921C4 090XF0 09JL77
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424 421.5 420.5 420.5 419.5 419.5 419.5 410.5 400.5 400.5 400.5 400.5 400.5 393.5 393.5	389.5 388.5 388.5 383.5
L1112222222222222222222222222222222222	0 4 4 4 4 4 0 1 0 0 1 0 0 4 0 0 0 0 0 0
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### ALIGNMENTS

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			, te)	•		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Sciurognathi; Muridae; Murinae; Mus				tabases.												CRC64;	Length 468;	Indels 4;	1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP	
	468 AA.	17, Created)	(Trembirel. 21, Last sequence update)	ene.		iata; Vertebra	rognathi; Muri				Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases												WN_1. 96352328B3332ADB CRC64;	Score 589; DB 11;	Pred. No. 7.4e-50; 9; Mismatches 13;	LVKPGASVKLSCTA	:  :
	Y; PRT;		. 21, Last a	Similar to RIKEN cDNA 1810060009 gene.		ordata; Cran	Rodentia; Sciu				o the EMBL/G	/8.1;		1g.	19-01.	tg_tike.	19_MHC.			3.		e; 1.	0			NSEVOLOOSGAE	NSEVQLQQSGAE
	PRELIMINARY	(TrEMBLrel.	2 (TrEMBLrel	RIKEN CDNA	Mus musculus (Mouse).	Metazoa; Ch	ed 		ROM N.A.	R.;	(FEB-2001) t	EMBL; BC0038/8; AAH038/8.1;					TPR003006; I		0409; IG; 2.	SM00407; IGc1;	SMART; SM00406; IGv; 1.	0410; IG_11k	S00290; IG_MHC; UNKN 468 AA; 51661 MW;		milarity 8 Conservati	VMFFLMAVVTGV	:         VIFFLMAVVIGV
JLT 1	Q99L31 Q99L31;	01-JUN-2001	01-JUN-2002	Similar to	Mus muscul	Eukaryota;	Mammalia; Eutheria; NCBI TaxID=10090;	[1]	SEQUENCE FROM N.A.	Strausberg R.;	Submitted	EMBL; BCCC.	HSSP; PU1842; /FAB.				InterPro;			SMART; SMO(	SMART; SMO(	SMART; SMO(	PROSITE; PS SEQUENCE	Query Match	Best Local Similarity 81. Matches 114; Conservative	1 MKCSW	1 MKCSW
RESULT 099L31	K D	TO	2 5	Œ	os	ပ္ပ	8 8	R.	ЯÞ	RA	Z.	D.K	Z i	Z 2	ž	ž č	ž 2	Z Z	DR.	DR	DR	DR	S OR	ã	ďΣ	ΟŽ	QQ

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SEQUENCE
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Q9D8L4
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61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                      61 EQGLEWIGWIDPEDGETKYAPKFQDKATITADTSSNTAYLQLSSLTSEDTAIYYCARNLL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888; AAH03888.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; 1g; 3.
SMART; SM00409; IG; 2.
SMART; SM00409; IGc1; 3.
SMART; SM00410; IGc1; 3.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 473 AA; 52449 MW; BE98B9B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                  099125;
099125;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
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                                                                                     121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                           121 YGGY----YDYWGQGTTITV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003500; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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Matches
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Carralnesses, School Carrange 
                                                                                                                                      streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 AELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPKFQGKA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomí;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
9
                                            Malkiel S., Liao L., Cunningham M.W., Diamond B.; "T-Cell-dependent antibody response to the dominant epitope of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 TITADISSNTAYLQLSSLTSEDIAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
64.3%; Score 480; DB 11; Length 109;
Best Local Similarity 80.5%; Pred. No. 7.1e-40;
Matches 91; Conservative 8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;
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01-000-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
181006600981k protein.
IGH-1 OR 1810060009RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 8
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                                                                                                                                                                                                                     Infect. Immun. 98:3803-5808(2000).
EMBL; AF206021; AAF69319.1; -
HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
Ffan; PF00047; ig; 1.
NON_TER
MEDLINE=20448942; PubMed=10992488;
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EMBL; AK007918; BAB25349.1; -.

HSSP; P01842; FAB.

MGD; MGI:96443; Igh-1.

InterPro; IPR003599; Ig.

InterPro; IPR003597; Ig_c1.

InterPro; IPR003507; Ig_like.

InterPro; IPR003606; Ig_like.
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092403;
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     RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GHGLEWIGEILDESGSTNYNEKFKGKATFTADISSNTAYMQLSSLTSEDSAVYXCAR--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                    61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TEMBLrel. 20, Last sequence update)
01-MAR-2002 (TEMBLrel. 21, Last annotation update)
Hypothetical 67.9 kba protein.
Mus musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Musculus                                                                                                                                                                                                                                                                            4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO18315; AAH18315.1; -.
InterPro: IPR003599; Ig.
R InterPro: IPR003509; Ig.—M.C.
R InterPro: IPR003506; Ig.—M.C.
R InterPro: IPR003566; Ig.—W.
R Pfam; PF00047; Ig.; 5.
R SMART; SM00409; IG; 2.
R SMART; SM00409; IG; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                   f Match 64.1%; Score 478; DB 11; Length 4 Local Similarity 67.1%; Pred. No. 6.8e-39; nes 94; Conservative 19; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;
                         PFGMT; PF00047; 1g; 4.

SMART; SM00409; 1G; 2.

SMART; SM00406; 1Gv; 1.

SMART; SM00410; 1G_L; 3.

SMART; SM00410; 1G_L; 1.

SMART; SM00410; 1G_MHC; 1.

SMART; SM00410; 1G_MHC; 1.

SMART; SM00410; 1G_MHC; 1.

SMART; SM00410; 1G_MHC; 1.

SEQUENCE 473 AA; 51699 MW; 9DED57AS14475FBB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00290; IG_MHC; UNKNOWN_3.
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121 --DYDWFA--YWGQGTLVTV 136
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Matches 87; Conservative
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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TISSUE=SALIVARY GLAND;
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Best Local S
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                                                                                                                                                                                                                                                                        Matches
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80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kozono Y., Kozono H., Azuma T.;
Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl) Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067797; BAB63282.1;
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 1.
NON_TER
                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 59.4%; Score 443; DB 11; Length 146; Best Local Similarity 71.1%; Pred. No. 4.6e-36; Matches 86; Conservative 14; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO18322; AAH18322.1;
MGD; MGI:2144917; AI893585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER 146 146
SEQUENCE 146 AA; 16136 MW; CEA8DD6E1955807F CRC64;
                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
14-Ppothetical 53.2 kba protein.
AI895585.
  146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR00359; Ig.
InterPro; IPR00359; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_wHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00409; IG; 3.
SMART; SM00400; IG; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                            STRAIN-C57BL/6;
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          RESULT 9
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                                                                                                                                                                                                                                                              61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                             61 EQGLEWIGRIDPANGYTKYDPKFQCKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                        5;
                                                                      58.8%; Score 439; DB 11; Length 489; 62.7%; Pred. No. 5.1e-35; ive 16; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.6%; Score 437; DB 11; Length 168; 60.6%; Pred. No. 2.1e-35; ive 19; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ416332; CAC94867.1; -.
Interpro; IPR003599; Ig.
Interpro; IPR003599; Ig.MHC.
Interpro; IPR003596; Ig.MHC.
Interpro; IPR003596; Ig.V.
Interpro; IPR001309; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chernajovsky Y.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
  11 protein.
489 AA; 53208 MW; CC85B1194DAFEF2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel, 20, Created)
01-MAR-2002 (TrEMBLrel, 20, Last sequence v
01-JUN-2002 (TrEMBLrel, 21, Last annotation
Anti-MOG 212 variable gamma 2a (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00294; PRENTLATION; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Targeting T cells to the CNS.";
                                                                                                                                                                                                                                                                                                                                                              121 YGNY-GVYA-MDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                         121 RGNYDGSLAWFVYWGQGTLVTV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YGNYGV--YAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --NYGSSRWYFDVWGAGTTVTV 136
                                                                                                                   89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                      Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BALB/C;
Hypothetical SEQUENCE 46
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sembi P.;
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Best Local S
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                                                                                                                      Matches
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61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSDY--DYD-YAMDYWGQGTSVT 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                  Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB067785; BAB63270.1;
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C57BL/G,

KOZONO Y., KOZONO H., Azuma T.;

KOZONO Y., KOZONO H., Azuma T.;

KOZONO Y., KOZONO H., Azuma T.;

Fortect Estination of Relative Affinity by Flow Cytometry Reveals

Affinity Maturation of B Cell Antigen Receptors in Response to (4-

Hydroxy-3-Nitrophenyl)Acetyl (NP).";

Submitted AGG-2001) to the EMBL/GenBank/DDBJ databases.

InterPro, IPR003006; Ig_MHC.

Pfam; PF00047; ig; 1.

NON_TER 15

NON_TER 145

SEQUENCE 145 AA; 15979 MW; 0162D0A26C746C04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.8%; Score 431.5; DB 11; Length 145; 70.2%; Pred. No. 6.2e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 70.2%; Pred. No. 6.2e-35;
Matches 85; Conservative 14; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
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Pred. No. 6.2e-35;
        145 AA.
                                                                                                                                  VH186.2-D-J-C mu protein (Fragment).
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.8%;
69.4%;
     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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01-DEC-2001 (
01-DEC-2001 (
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Q924R4
Q924R4;
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61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                     1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kozono Y., Kozono H., Azuma T.;

Kozono Y., Kozono H., Azuma T.;

Affinity Estimation of Relative Affinity by Flow Cytometry Reveals

Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Mitrophenyl) Acetyl (NP).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

Babbiz, ABO67794; Babb3279.1;

InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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                                                                                                                                                                                                       Query Match 57.2%; Score 426.5; DB 11; Length 488; Best Local Similarity 59.6%; Pred. No. 8.6e-34; Matches 84; Conservative 21; Mismatches 35; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 57.0%; Score 425.5; DB 11; Length 145; 1 Similarity 68.3%; Pred. No. 2.4e-34; 84; Conservative 14; Mismatches 18; Indels 7;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC01539; ARH13399.1; -. MGD; MGI:2144917; AI893585. InterPro; IPR003006; Ig_MHC.
                                                                                 Pfm: FP00047; 1g; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 AA; 16011 MW; 9BC0846D40DF97EA CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   463 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 YGNYGVYAM-DYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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VTV 118
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                                                                                                                                                                   65 EWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNY 124
    3; Gaps
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                                                                        5 WVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGL 64
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 52.1 kDa protein.
Hypothetical 52.1 kDa protein.
Buka musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 57.5%; Score 429; DB 11; Length 481; Best Local Similarity 61.8%; Pred. No. 4.8e-34; Matches 84; Conservative 16; Mismatches 30; Indels 6
    21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BCO19490; ARH13490.1; -
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; 1g; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothatical protein.
SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNU-2002 (TrEMBLrel. 21, Last annotation update)
A1893585.
                                                                                                                                                                                                                                                                                                                                                                                                481 AA.
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       13; Mismatches
    84; Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
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Strausberg R.;
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091WR1
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                                                                                         Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 57.0%; Score 425.5; DB 11; Length 463; Best Local Similarity 59.3%; Pred. No. 1e-33; Matches 83; Conservative 21; Mismatches 33; Indels 3;
                                                                                                                                                                                                                                              | MGD; MGI:96446; 1gh-4. |
| MGD; MGI:99646; 1gh-4. |
| InterPro; IPR003599; 1g. |
| InterPro; IPR003600; 1g_like. |
| InterPro; IPR003006; 1g_lke. |
| InterPro; IPR003006; 1g_lke. |
| InterPro; IPR00356; 1g_w.c. |
| InterPro; IPR00356; 1g_w.c. |
| InterPro; IPR0040; 1g, 4. |
| SMART; SM00409; 1G; 2. |
| SMART; SM0040; 1G_like; 1. |
| SMART; SM00410; 1G_like; 1. |
| PROSITE; PS00290; IG_MHC; UNKNOWN_1. |
| PROSITE; PS00290; IG_MHC; UNKNOWN_1. |
| SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64; |
                                                                                                                                                                                     Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003435; AAH03435.1; -
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013488; AAH13488.1;
MGD; MGT2144917; AI893585.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      091WT3;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UJUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.0 kDa protein.
AI893585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE, PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein; Immunoglobulin domain.
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| 121 Y-SYDLFA--YWGQGTLVTV 137
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January 6, 2003, 12:46:55; Search time 24.6263 Seconds (without alignments) 573.557 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pineseq_101002:*  //SIDS2/gcddata/geneseq/geneseqp-embl/AA1980.DAT:* //SIDS2/gcddata/geneseq/geneseqp-embl/AA1981.DAT:* //SIDS2/gcddata/geneseqy-embl/AA1981.DAT:* //SIDS2/gcddata/geneseqy-embl/AA1981.DAT:* //SIDS2/gcddata/geneseqy-embl/AA1983.DAT:* //SIDS2/gcddata/geneseqy-embl/AA1985.DAT:* //SIDS2/gcddata/geneseqy-embl/AA1986.DAT:* //SIDS2/gcddata/geneseqy-embl/AA1980.DAT:* //SIDS2/gcddata/geneseqy-embl/AA1980.DAT:* //SIDS2/gcddata/geneseqy-embl/AA1980.DAT:* //SIDS2/gcddata/geneseqy-embl/AA1989.DAT:* //SIDS2/gcddata/geneseqy-embl/AA1989.DAT:* //SIDS2/gcddata/geneseqy-embl/AA1999.DAT:* //SIDS2/gcddata/geneseqy-embl/AA2001.DAT:* //SIDS2/gcddata/geneseqy-embl/AA2001.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			Description	Humanized anti-VLA	Humanised alpha-4	Humanised alpha-4	Mouse anti-VLA-4 a	Mouse VLA-4 antibo	Human VLA-4 reshap	Alpha-4 integrin m	Human MCP-3 and mu	Human IP-10 and mu	Artificial synthet
		1	an Tarangan	AAR81321	AAW22412	AAW22419	AAR81328	AAR81326	AAR81332	AAW22409	AAY29913	AAY29911	AAY29916
			08	16	18	18	16	16	16	18	20	20	20
		:	Length	106	106	126	106	126	126	126	359	361	374
	æ	Query	e Match Length DB ]	100.0	100.0	100.0	90.4	90.4	90.4	90.4	86.8	86.8	86.8
		1	Score	562	562	562	508	208	208	208	488	488	488
		Result	So	ī	7	m	4	S	9	7	80	6	10

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           variable region, La, directed against leukocyte adhesion molecule
variable region, La, directed against leukocyte adhesion molecule
VLA-4. Cloned CDNA sequences of mouse 21.6 VL and VH (AAQ99889 and
AAQ99829. regions are linked to human constant regions in the
construction of a humanized antibody against VLA-4. The 5' and 3'
ends of the mouse cDNAs are modified using PCR primers (See
AAQ9989-289) and then subcloned into mammalian cell expression vectors
containing human kappa or gamma-1 constant regions. In the humanized
light chain, amino acids L45, L58 and L69 in the humanized
containing human kappa or gamma-1. L49, L58 and L69 in the humanized
light chain, amino acids L45, L58 and L69 in the humanized
containing human kappa or gamma-1.

Containing human kappa or gamma-1.

PR framework are replaced by the amino acid present in the equivalent
position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric
antibodies are transfected into COS cells. The humanized antibodies
can be used for inhibiting adhesion of a leukocyte to an endothelial
cell and for treating inflammatory diseases such as multipple
sclerosis. They can also be used in the treatment of stroke,
cerebral traumas, meningitis or encephalitis. The antibodies can
also be used for detecting VLA-4, for affinity purification or for
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                                                                                                        The sequence encodes the humanized mouse antibody 21.6 light chain
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/label= CDR1
/note= "21.6 complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma: atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 562; DB 16; Length 106; 100.0%; Pred. No. 1.2e-36; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "REI Lys-45 is substd. by Lys of mouse 21.6 VL, important in supporting the CDR2 loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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/note= "RE1 framework region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             generating anti-idiotype antibodies.
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                                 Claim 9; Page 67; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-DEC-1997 (first entry)
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Chimeric Homo sapiens;
Chimeric synthetic.
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This polypoptide, designated La, comprises the light chain variable region (VL) of a humanised alpha-4 integrin antibody 21.6. It is composed of complementarity determining regions (CDRs) from the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody al.6 and a modified human REI framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate fragments of mouse and human DNA sequences. The humanised 21.6 VL and a humanised 21.6 VK and a humanised 21.6 VL and be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to produce a claimed humanised 21.6 antibody that its useful in the manufacture of a medicament for treating asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, theumatoid ischaemia, and acute leukocyte mediated lung injury. The antibody for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
                                                                                                                                             "21.6 complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "21.6 complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                  /note= "REI Val-58 is substd. by Ile of mouse 21.6 VL, important in supporting the CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "REI Thr-106 substd. by Lys, more typical of human kappa light chain J region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "REI Leu-103 substd. by Val, more typical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "REI Gln-104 substd. by Glu, more typical of human kappa light chain J region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "REI Thr-69 is substd. by Arg of mouse 21.6 VL, involved in antibody-antigen binding"
/note= "REI Tyr-49 is substd. by His of mouse 21.6 VL, located at the binding site"
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/label= FR3
/note= "REI framework region 3"
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                                                                                                              /label= CDR2
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/label= FR4
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                                              1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                         1 DIQMIQSPSSLSASVGDRVITTCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "21.6 complementarity determining region 1"
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/note= "21.6 complementarity determining region 3"
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                                                                                                                                                                                                                                                           Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
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 Length 106;
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                                                                                        RESGSGSGRDYTFIISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                       Humanised alpha-4 integrin antibody 21.6 VL version La.
                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Mat_protein
/note= "VL version La (Claim 25)"
100.0%; Score 562; DB 18;
100.0%; Pred. No. 1.2e-36;
ive 0; Mismatches 0;
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/note= "REI framework region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "REI framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                      AAW22419 standard; Protein; 126 AA
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                                                                                                                                                                                                                                                                                                                                                                                                           /label- Leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CDR1
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                       Conservative
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Chimeric Homo sapiens;
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                                                                                                                                                                                                                                                                                                                                                              Chimeric synthetic.
            Similarity
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            Best Local Sim
Matches 106;
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   Query Match
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This polypeptide, designated La, comprises the light chain variable region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also AMV22412). It is composed of complementarity determining regions from the VL region (see AMV22409) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human REI framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate mouse and human DNA sequences. The humanised 21.6 VL and a humanised 21.6 VH (see AMV22413) can be used to produce a claimed humanised 21.6 antibody that is useful in the manufacture of a medicament for treating asthma, atherosclerosis, contrictis, transplant rejection, graft versus host disease, theumatic metastasis, nephritis, atopic dermatitis, psoriasis, mycoardial ischemia, and acute leukocyte mediated lung injury. The humanised antibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "mouse light chain variable complementarity determining region 1"
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                                                              Uses of humanised alpha-4 integrin antibody - for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 562; DB 18; Length 126; 100.0%; Pred. No. 1.4e-36; Live 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse anti-VLA-4 antibody 21.6 light chain variable region.
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                                                                                                             Example 6; Fig 10; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          region 2
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/label= CDR1
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/label= FR2
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/label= FR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody engineering.
             WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  126 AA;
                               N-PSDB; AAT74788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR81328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain variable region (without signal sequence). Cloned cDNA CDR sequences of mouse 21.6 variable light and variable heavy regions are linked to human constant framework regions of the REI antibody for the light chain and the 2*CL antibody gainst VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LCWR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig light contain the humanized antibodies are transfected into COS acid present in the equivalent position of the mouse 21.6 Ig light colain. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple solerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.
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                                                                                                        /note= "mouse light chain variable complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                            /note= "mouse light chain variable framework region 3"
                                                                                                                                                                        /note= "mouse light chain variable framework
region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dery Match 90.4%; Score 508; DB 16; Length 106; st Local Similarity 88.7%; Pred. No. 1.8e-32; tches 94; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bendig MM, Jones TS, Leger OJ, Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 66; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                         /label= CDR3
57..88
/label= FR3
                                                                                                                                                                                                                                                                                                                                             94US-0186269
                                                                                                                                                                 /label= FR4
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                                                                                                                                              901..76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammatory disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 AA;
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The sequence represents the mouse antibody 21.6 light chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned CDNA sequences of mouse 21.6 VL and VH (see AAQ9892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ9895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids LA5, L49, L58 and L69 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 fl Chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                           Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for
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                                                                                                                                                                                                                             "complementarity determining region 1" \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                          "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                       "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.4%; Score 50%; DB 16; Length 126; 88.7%; Pred. No. 2.2e-32; Live 6; Mismatches 6; Indels
                            Mouse VLA-4 antibody 21.6 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leger OJ, Saldanha J;
                                                                                                                                                                                                                                                                                                    /note= "framework region 3"
                                                                                                                                                                                                                                                                                                                                                                 ...126
+-- "framework region 4"
                                                                                                                                                                                                "framework region 1"
                                                                                                                                                                                                                                                            "framework region 2"
                                                                                                                                                                   /note= "signal peptide"
                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ATHE-) ATHENA NEUROSCIENCES INC.
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 23-MAR-1996 (first entry)
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Best Local Similarity 88.73
Matches 94; Conservative
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117..12
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                                                                             antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-269276/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ99889
                                                                                                                                                                                                                                                                                                                                                                                                                 WO9519790-A1.
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                                                                                                         Mus musculus.
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AAR81326 standard; Protein; 126 AA.

**AAR**81326

AAR81326

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21-NOV-1996;
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          21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
DIOMIQSPSSLSASVGDRVIITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                               Humanized antibody; leukocyte adhesion molecule; {\tt VLA-4}; therapeutic; antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain variable region against leukocyte adhesion molecule VLA-4.
Cloned CDNA sequences of mouse 21.6 VL (AAQ99889) and VH (AAQ99892)
regions are linked to human constant regions in the construction
of a humanized antibody against VLA-4. The 5' and 3' ends of the
mouse cDNAs are modified using PCR primers (See AAQ99895-98) and
then subcloned into mammalian cell expression vectors containing
human kappa or gamma-1 constant regions. In the humanized light
chain, amino acids LAS, L49, L58 and L69 in the human kappa LC VR
framework are replaced by the amino acid present in the equivalent
                                                                                                                                                              Human VLA-4 reshaped antibody 21.6 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents the human reshaped antibody 21.6 light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                      "complementarity determining region 1"
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                                                                                                                                                                                                                                                                                                                                                                 "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                  70..76 // note= "complementarity determining region
                                     RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                               Jones TS, Leger OJ, Saldanha J;
                                                                                                                                                                                                                                                                                                                                   ..108
ote= "framework region 3"
                                                                                                                                                                                                                                                                  "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                         117.126
/note= "framework region 4"
                                                                                                                                                                                                                                                                                                        'note= "framework region 2"
                                                                                                                                                                                                                                                /note= "signal peptide"
                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                     AAR81332 standard; Protein; 126
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                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory disease.
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                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                           23-MAR-1996
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                                                                                                                        AAR81332;
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Gaps
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                chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an antibodies can be used to train inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, menigitis or encephalitis. The antibodies can also be used for detecting VLA 4, for affinity purification or for generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            asthma, atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "complementarity determining region 1"
  Plasmids encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "complementarity determining region 2"
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/note= "complementarity determining region 3"
                                                                                                                                                                                                                                                      Length 126;
                                                                                                                                                                                                                                                                                               6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      90.4%; Score 508; DB 16;
88.7%; Pred. No. 2.2e-32;
live 6; Mismatches 6;
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/label= FR4
/note= "framework region 4"
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position of the mouse 21.6 Ig L chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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/label= CDR2
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/label= CDR1
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Matches 94; Conservative
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/label= 1
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/label= 1
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                                                                                                                                                                                                          Sequence
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96WO-US18807

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine; immune response; HIV; infection.
                                                                                                                                                                                                                                                                                                 This polypeptide comprises the light chain variable region (VL) of mouse anti-alpha-4 integrin monoclonal antibody 21.6. The complementarity determining regions (CDRs) of the 21.6 VL can be incorporated into a human REI framework to produce a claimed humanised 21.6 VL (see AAW22412) and a claimed humanised 21.6 vL (see AAW22412) and a claimed humanised 21.6 antibody that is used in the manufacture of a medicament for treating a disease selected from asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour metantic, and the contraction of the contraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metastasis, nephritis, journelly partitives incommetastasis, nephritis, atopic dermattis, psoriasis, myocardial ischaemia, and acute leukcoyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin for use as a vaccine or an immunogen. It is also useful for expensating idiotypic antibodies. The humanised antibodies of the quivention have a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
;
                                                                                                                                                                                                     Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 126;
                                                                                                  Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.4%; Score 508; DB 18;
88.7%; Pred. No. 2.2e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human MCP-3 and murine scFv38 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY29913 standard; Protein; 359 AA
                                                                                                                                                                                                                                                                 Claim 18; Page 68; 107pp; English.
                                                         (ATHE-) ATHENA NEUROSCIENCES INC
                   95US-0561521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0077745.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94; Conservative
                                                                                                                                         WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 AA;
                                                                                                                                                              N-PSDB; AAT74759
                   21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09946392-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-SEP-1999.
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY29913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
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The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein.3 (WCP-3) and human monocyte chemotactic protein.3 (WCP-3) and human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (3) human Muc-1; (5) human PDC and HIV gpl20; and HIV gpl20; (6) human MCP-3 and HIV gpl20; (7) human MCP-3 and HIV gpl20; and (8) human SDF-1 and HIV gpl20; (7) human MCD and HIV gpl20; and elso proteins and nucleotide sequences encoding them, can be used for producing an immune response, e.g. an effector T cell immune response. They can also be used for tracting cancer or treating or preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in screening assays. Con identifying unknown tumour antigen epitopes and fine mapping of trumour antigen epitopes. The present sequence represents a fusion protein contact invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó;
                                                                                                                                New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20; Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLEIK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 488; DB 2(
Pred. No. 2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human IP-10 and murine scFv38 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                 Disclosure; Page 118-119; 142pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY29911 standard; Protein; 361 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune response; HIV; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.8%;
84.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US05345.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.9°
Matches 90; Conservative
Kwak LW, Biragyn A;
                                                                  WPI; 1999-551418/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kwak LW, Biragyn A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-551418/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09946392-A1.
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Synthetic.
                                                                                                                                                                                                      infection
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New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
            infection
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Disclosure; Page 115-116; 142pp; English.

and a tumour antigen or HTV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human Muc-1: (2) human interferon-induced protein 10 (1p-10) and human Muc-1: (3) human macrophage-derived chemotine (MDC) and human Muc-1: (4) human SDF-1 and human Muc-1: (4) human EDF-1 and human Muc-1: (4) human EDF-1 and HTV gpl20: (6) human MCP-3 and HTV gpl20: (7) human MDC and HTV gpl20: and (8) human SDF-1 and HTV gpl20: (7) human MDC and HTV gpl20: and (8) human SDF-1 and HTV gpl20: The fusion proteins, and nucleotide sequences encoding them, can be used for producing an immune response. e.g. an effector T cell immune preventing HTV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in screening assays for identifying unknown tumour antigen epitopes and fine mapping of furner the mathem epitopes. The present sequence represents a fusion protein present invention describes fusion proteins comprising a chemokine from the present invention.

361 AA; Sequence

ö 0; Gaps DB 20; Length 361; Indels 7; 86.8%; Score 488; DB 20 84.9%; Pred. No. 2e-30; iive 9; Mismatches Matches 90; Conservative Similarity Query Match Local

235 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 294 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60 ŏ g

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AAY29916 standard; Protein; 374 17-NOV-1999 AAY29916; RESULT 10 **AA**Y29916 

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Artificial synthetic construct protein SEQ ID NO:15. (first entry)

tumour; viral; antigen; fusion protein; cancer; vaccine; immune response; HIV; infection Chemokine;

Synthetic

W09946392-A1

16-SEP-1999

99WO-US05345. 12-MAR-1999;

98US-0077745. 12-MAR-1998; (USSH ) US DEPT HEALTH & HUMAN SERVICES

Kwak LW, Biragyn A;

WPI; 1999-551418/46.

fusion polypeptides comprising a chemokine and a tumour antigen or antigen, used for treating cancers or treating or preventing HIV infection

Disclosure; Page 117-118; 142pp; English.

present invention describes fusion proteins comprising a chemokine The

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and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human Muc-1; (2) human interferon-induced protein 10 (1P-10) and human Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human Muc-1; (5) human IP-10 and HIV gpl20; (6) human MCP-3 and human Muc-1; (5) human IP-10 and HIV gpl20; (6) human MCP-3 and human Muc-1; (5) human IP-10 and HIV gpl20; (6) human MCP-3 and hiv gpl20. The fusion proteins, and nucleotide sequences encoding them, fammine response. They can also be used for treating cancer or treating or preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in ordenting assays for identifying unknown tumour antigen epitopes. ANZ21166 are sequences given in the SEQ ID LISTING in the present invention but which
                                                                                                                                                                                                                                                                                                                                                                   95 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAMYQHKPGKGPRLLIHYTSTLQPGIPS 154
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                      9
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or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of the MEI-14 light chain. The protein monoclonal antibody which can be administered to treat solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         administering monoclonal antibody Mel-14, having Fc deleted, using injection or deposition in the cyst cavity
                                                                                                                                                                                                                                                                                     Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Method of treating solid or cystic tumours with antibodies
                                                                                                                                                                                                                                                                                                                     7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                          are not mentioned further within the specification.
                                                                                                                                                                                                                                                                                     Score 488; DB 20;
Pred. No. 2.1e-30;
                                                                                                                                                                                                                                                                                                                     9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ME1-14 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zalutsky MR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR60627 standard; Protein; 128
                                                                                                                                                                                                                                                                                     86.8%;
84.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-US02724.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monoclonal antibody; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JUN-1995 (first entry)
                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 84.9
Matches 90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-316669/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIGNER D D.
                                                                                                                                                                                                                                                         374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    See also AAR60626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ73537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cystic tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR60627;
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(CARR/)
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                             Gaps
                                         1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                 21 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLMHYTSTLQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New CD4 specific recombinant - complementarity determining region grafted antibody for treating graft rejection and T cell disorders
                             ;
               Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jolliffe LK, Zivin RA, Pulito VL, Adair JR, Athwal DS;
                            8; Indels
                                                                      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                             variable region; antibody; OKT4A; heavy chain; CD4; complementarity determining region.
             85.6%; Score 481; DB 15;
84.0%; Pred. No. 2.7e-30;
ive 9; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                        133..234
/label= kappa constant domain
                                                                                                                                                                                                                                       1..45
|abel= framework region 1
                                                                                                                                                                                                                                                                                              77..110
/label= framework region 3
                                                                                                                                                                                                                                                                                                                                  /label= framework region 4

    3..69
    label= framework region

                                                                                                                                                                                                                          ...20
Tabel= signal sequence
                                                                                                                                                                 CD4-specific CDR-grafted light chain.
                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                       AAR13050 standard; Protein; 234 AA.
                                                                                                                                                                                                                                                                                  70..76
/label= CDR 2
                                                                                                                                                                                                                                                            label= CDR 1
                                                                                                                                                                                                                                                                                                                    label= CDR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 8; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        89GB-0028874.
90WO-GB02017.
                                                                                                                                                                                                                                                                                                                                                                                          90WO-GB02015.
                                                                                                                                                                                                                                                                                                                                                                                                                      90WO-GB02018
                                                                                                                                                  27-SEP-1991 (first entry)
                   Local Similarity 84.0 es 89; Conservative
                                                                                                                                                                                                                                                                                                                           ..132
                                                                                                                                                                                                                                                                                                                                                                                                                                    (ORTH ) ORTHO PHARM CORP.
                                                                                                                                                                                                                                                                                                             ..116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1991-222914/30.
128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ12633.
                                                                                                                                                                                                                                                                                                                                                              WO9109966-A.
                                                                                                                                                                                                                                                                                                                                                                                           21-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                      21-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                            11-JUL-1991
Sequence
                                                                                                                                                                                                    Synthetic.
                                                                                                                                     AAR13050;
             Query Match
                                                                                                                                                                                                                         Peptide
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Hybridoma antibodies have been produced with the spleen cells of BALB/c mouse that had received multiple injections of mercuric ions reacted with glutathione to produce a mercuric ion coordinate covalent compound which was covalently bound to keyhole limpet hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5, 5B6 and 3E8) were producing Mabs that were strongly positive against glutatione-mercuric ions but negative against glutathione without mercuric ions. RNA was isolated from hybridoma cells with guanidine isothiocyanate. First strand cDNA synthesis was catalysed by MuLv reverse transcriptase. The primers used for cDNA synthesis were complementary to the 5' end of the CH1 domain of the heavy creat newscriptase. The primers used for cDNA synthesis are chain expressed by the hybridoma of interest, or to the 5' and of che chain expressed by the primers used for cDNA synthesis are shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide(s) which bind heavy metals, esp. mercury - derived from monoclonal antibodies, used for detecting, removing, adding or
This is an example of a CDR-grafted light chain of the invention. The constant regions are based on sequences of the human kappa constant domain, the signal sequence is derived from murine MAD B72.3 and the CDR sequences are based on the murine OKT4A light chain CDRs. The recombinant antibody encoded by this sequence has affinity for CD4 similar to that of OKT4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 DIQMTQSPSSLSASVGDRVTITCKASPDINNYLNWYQQTPGKAPKLLIYYTSTLQPGVPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody; heavy metal; mercury; variable region;
                                                                                                                                                                                                                                                                                                                                                                       84.6%; Score 475.5; DB 12; Length
84.9%; Pred. No. 1.3e-29;
ive 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain variable region for monoclonal antibody 23F8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 23; Page 67-68; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR78970 standard; Protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lopez O, Wagner FW, Wylie DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-0187407.
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 84.99
"a+rhes 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neutralising heavy metals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BION-) BIONEBRASKA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-275415/36.
N-PSDB; AAQ97508.
                                                                                                                                                                                                                                                                                                 234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-1995.
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                                                                                                                                                                                                                                                                                                     Sequence
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(PROT-) PROTEINE PERFORMANCE SA.

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variable region of a particular antibody polypeptide was also used for PCR amplification of that variable region, in conjunction with an appropriate V-region primer. In addition, the VH primer AAQ97518 was used to amplify the mAD 2D5 and 5B6 heavy chains. The sequences of the PCR amplified nucleotides were determined. These are given in AAQ9789-097510 and the deduced AA sequences in AAR7941-R79250 & AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45 and in the claims are different from the descriptions in the sequence listings. The descriptions in the sequence listings are
                                                                                                                                                                                                                                             1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60
                                                                                                                                                                                                                             1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD29;
                                                                                                                                                                                                    ;
                                                                                                                                                                           DB 16; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody; light chain; kappa; variable region; K20; integrin; beta 1 subunit; humanisation; Hu-K20; immunosuppressant; T cell activation; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine monoclonal antibody K20 kappa chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "complementarity determining region"
                                                                                                                                                                                                                                                                                  RFSGSGSGRDYTFIISSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                Score 471.5; DB 16;
Pred. No. 1.3e-29;
9; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "framework region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "framework region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "framework region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/label= J_kappa1
                                                                                                                                                                                                                                                                                                                                                                            AAR93159 standard; Protein; 108
                                                                                                                                                                                                   6
                                                                                                                                                                          83.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4..34
'label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94FR-0010858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94FR-0010858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                 24-OCT-1996 (first entry)
                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                     Local Similarity
Les 89; Conserv
                                                                                                                                                107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                 Sequence
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                                                                                                                                                                           Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                          The present sequence is that of the variable region of the kappa light chain from murine monoclonal antibody K20. The antibody recognises the beta 1 subunit (CD29) of integrins and inhibits activation and proliferation of peripheral T cells induced by anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target for humanisation; the humanised version may be useful as an immunosuppressant. In the humanisation process, the complementarity
                                                                                                                                                                                                                                                                                             determining regions (CDRs) of a human antibody with framework regions 70-95% homologous to those of K20 were replaced by the K20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expression vectors for producing chimeric monoclonal antibodies - which express human constant region and non-human variable region
                                                                                                           Humanisation of non-human immunoglobulin variable regions - for
prodn. of humanised antibodies, esp. K20, e.g. as an
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
                                                                                                                                                                                                                                                                                                                                                                                  Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                            Margaritte
                                                                                                                                                                                                                                                                                                                                                                                 82.7%; Score 465; DB 17;
81.1%; Pred. No. 4.1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Variable region of murine AHT 107 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                             10; Mismatches
                            Lefranc MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR06252 standard; protein; 128 AA.
                                                                                                                                                                  Example 1; Fig 2A; 39pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89US-0441702.
89US-0301216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-DEC-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             86; Conservative
                          Cervoni MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1990-232892/31
                                                                 WPI; 1996-162083/17
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                      108 AA;
                                                                                                                                       immunosuppressant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ05556
                                                                                 N-PSDB; AAT26849
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24-JAN-1989;
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                          Bernard A,
                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                       Poul MA;
                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                            MAbs comprising mouse CH and CL constant regions whith human variable regions may be used to create mouse/human hybrid Mabs, which have a longer serum half-life. Method can be used to produce Abs against interleukin-2 receptor and tumour necrosis factor.
                                                                                                                                                                                                       1;
                                                                                                                                                             Odery Match 81.9%; Score 460.5; DB 11; Length 128; Best Local Similarity 76.6%; Pred. No. 1.1e-28; Matches 82; Conservative 18; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                                                                          Search completed: January 6, 2003, 13:15:17
Job time : 25.6263 secs
   Disclosure; ; p; English.
                                                                                                                             Sequence 128 AA;
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January 6, 2003, 13:13:21; Search time 8.7798 Seconds (without alignments) 355.228 Million cell updates/sec
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562
1 DIOMIQSPSSLSASVGDRVT ......YCLQYDNLWTFGQGTKVEIK 106
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                   262574 seqs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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	SUMMARIES
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Result		a Ouerv			SOMMAKLES	
No.	Score	Match	Length	BB	DI	Description
П	562	100.0	106	7	US-08-561-521-7	Sequence 7, Appli
7	562	100.0	106	S	PCT-US95-01219-7	7,
٣	508	90.4	106	7	US-08-561-521-5	Ŋ
4	508	90.4	106	ស	PCT-US95-01219-5	5,
'n	508	90.4	126	7	US-08-561-521-2	7
9	508	90.4	126	7	US-08-561-521-15	Sequence 15, Appl
7	508	90.4	126	5	PCT-US95-01219-2	7
80	508	90.4	126	5	PCT-US95-01219-15	Sequence 15, Appl
6	481	85.6	128	-	US-08-339-582-4	4
10	471.5	83.9	107	7	US-08-888-366-22	22,
11	460	81.9	637	7	US-08-235-838-16	16,
12	460	81.9	637	7	US-08-465-473B-16	16,
13	455	81.0	241	7	US-08-235-838-11	Sequence 11, Appl
14	455	81.0	241	7	US-08-465-473B-11	11,
15	454.5	80.9	108	7	US-08-602-725-29	29,
16	453.5	80.7	107	7	US-08-561-521-8	8, A
17	453.5	80.7	107	S	PCT-US95-01219-8	8
18	451	80.3	355	æ	US-08-875-811-57	Sequence 57, Appl
19	448.5	79.8	107	7	US-07-934-373C-17	17,
20	448.5	79.8		m	US-08-437-642B-17	17,
21	448.5	79.8	107	4	US-08-146-206C-17	17,
22	448.5	79.8		ß	PCT-US93-07832-17	17,
23	444.5	79.1		7	US-07-934-373C-18	18,
74	444.5	79.1		æ	US-08-437-642B-18	18,
25	444.5	79.1		4	US-08-146-206C-18	18,
56	444.5	79.1	П	S	PCT-US93-07832-18	18
27	444.5	79.1	108	m	US-08-974-899-3	3, 7

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0; Gaps

Query Match
100.0%; Score 562; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.2e-45;
Matches 106; Conservative 0; Mismatches 0; Indels

Sequence 67, Appl Sequence 71, Appl Sequence 71, Appl Sequence 71, Appl Sequence 6, Appl Sequence 15, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 3, Appl	ainst Leukocyte and Crew Suite 2000	
1 US-08-137-117D-67 2 US-08-436-717-67 1 US-08-137-117D-71 2 US-08-137-117D-71 2 US-08-656-51-6 2 US-08-652-58-34 4 PCT-US95-01219-6 5 US-08-070-116A-7 2 US-08-116-247-9 2 US-08-116-247-9 2 US-08-116-247-9 2 US-08-116-268-2 2 US-08-116-268-2 3 US-08-146-206C-3 5 PCT-US93-078-373C-3 3 US-08-4146-206C-3 5 US-08-4146-206C-3 5 US-08-4146-206C-3 6 US-08-4146-206C-3 8 US-08-4146-206C-3 8 US-08-4146-206C-3 9 US-08-4146-206C-3 9 US-08-4146-206C-3 9 US-08-4146-206C-3	ALIGNMENTS  //8561521  y M.  ler J.  ler J.  lose  arran manized Antibodies Ag menized Antibodies Ag hesion Molecule VLA-4  sand Townsend Khourie  laza, Steuart Tower,  clisk disk elease #1.0, version  A:  US/08/186,269A  US/08/186,269A  US/08/186,269A  US/08/186,269A  SER:  15270-14  MATION:  600  3:  7:  S:  ids	
444.5 79.1 111 444.5 79.1 126 444.5 79.1 126 443.5 78.9 107 443.5 78.9 107 443.5 78.9 107 443.5 78.9 108 441.5 78.9 108 440.5 78.4 109 440.5 78.4 109 440.5 78.4 109 440.5 78.4 109	1 10. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	-521-7
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GENERAL INFORMATION:
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                 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYWAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                                                                                                                                                                                                APPLICANT: Bendig, Mary M.
APPLICANT: Beger, Olivier J.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SOUURCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                    61 RFSGSGSGRDYFFISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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APPLICATION NUMBER: PCT/US95/01219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 562; DB 5;
100.0%; Pred. No. 1.2e-45;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,233
REFERENCE/DOCKET NUMBER: 15270-14
TELECHONE: 415-543-9600
TELEFAX: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WWBER: PCT/US95/01219
25-JAN-1995
                                                                                                                                                                                                                                             Sequence 7, Application PC/TUS9501219 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 5, Application US/08561521
; Patent No. 5840299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 7:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 106 amino acids
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94105
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APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
ATTLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bendid, Mary M.
APPLICANT: Bendid, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Solver, Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.4%; Score 508; DB 2; Length 106; 88.7%; Pred. No. 1.3e-40; Live 6; Mismatches 6; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 STRY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                          Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-78n-1994
ATTORNEY/AGRWT INFORMATION:
NAME: Smith, William L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15270-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5, Application PC/TUS9501219 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Smith, William L. REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-543-5043 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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MOLECULE TYPE: protein
US-08-561-521-5
                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                94105
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PCT-US95-01219-5
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 88.73
Matches 94; Conservative
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                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-2
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; MOLECULE TYPE: protein
US-08-561-521-15
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CITY: San Francisco
STATE: California
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APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 106;
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One Market Plaza, Steuart Tower, Suite 2000
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 508; DB 5;
Pred. No. 1.3e-40;
6; Mismatches 6;
                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/186,269
FILING DATE: 25-TAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
RESIGNERATION NUMBER: 15270-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-08-561-521-2
; Sequence 2, Application US/08561521
; Patent No. 5840299
                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 90.4%;
Best Local Similarity 88.7%;
Matches 94; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
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MOLECULE TYPE: protein
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CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
ITILE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                           Length 126;
                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGRDYTFTISSLQPEDIATYXCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OFFWARE: PATENTING SYSTEM: PC_DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           Score 508; DB 2;
Pred. No. 1.6e-40;
                                                                                                                                                                                                                                                                                                          90.4%; Sco...
88.7%; Pred No. 1...
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/O8/186,269A
FILLING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION IRFORMATION:
TELEPHONE: 415-543-9600
                                              15270-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/561,521 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-561-521-15; Sequence 15, Application US/08561521
patent No. 5840299; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
NAME: Smith, William L. REGISTRATION NUMBER: 30,223 REFERENCE/DOCKET NUMBER: 15;
                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 15:
                                                                                                           TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 126 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 126 amino acids
amino acid
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COUNTRY: US
PCT-US95-01219-15
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                                                       0; Gaps
                                                                                        1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                               1 DIQMTQSPSSLSASILGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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              90.4%; Score 508; DB 2; Length 126;
88.7%; Pred. No. 1.6e-40;
Live 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.4%; Score 508; DB 5; Length 126; Best Local Similarity 88.7%; Pred. No. 1.6e-40; Matches 94; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                           61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15270-14
                                                                                                                                                                                                                                                                                                          Sequence 2, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30,223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 126 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Smith, William L. REGISTRATION NUMBER: 3(
                                                     94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             San Francisco
: California
              Query Match
Best Local Similarity
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PCT-US95-01219-2
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                                                     Matches
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RESULT 8

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Sequence 15, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
90.4%; Score 508; DB 5; Length 126;
Best Local Similarity 88.7%; Pred. No. 1.6e-40;
Matches 94; Conservative 6; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURREMY APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bigner, Darell D.
APPLICANT: Zalutsky, Michael R.
APPLICANT: Carrel, Stefan
TITLE OF INVENTION: METHOD OF TREATMENT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08339582
Patent No. 5558852
GENERAL INFORMATION:
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STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 5558852th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-960
TELEBRAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 126 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-15
                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        USA
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1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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Patent No. 5571894

GENERAL INFORMATION

APPLICANT: Wels, Winfried S.

APPLICANT: Harwerth, Ina-Maria

APPLICANT: Harwerth, Ina-Maria

APPLICANT: Hardman, No. 5571894man

APPLICANT: Bernd

APPLICANT: Bernd

APPLICANT: Bernd

APPLICANT: Groner, Bernd

APPLICANT: Groner, Bernd

APPLICANT: Grover, Markus

TITLE OF INVENTION: Recombinant Antibodies Specific for a TITLE OF INVENTION: Growth Factor Receptor

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIRA-GEGGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 107;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.9%; Score 471.5; DB 2;
83.2%; Pred. No. 3.4e-37;
7ative 9; Mismatches 8;
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION UNGER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.39USC1
TELECOMMUNICATION INFORMATION:
TELEFHONE: 612-332-5300
TELEFAX: 612-332-9081
                             APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PROR APPLICATION DATA:
APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989
ATTORNEY AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARE: PatentIn Palcas
                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: LENGTH: 107 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 83.29
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-888-366-22
       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-235-838-16
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Patent No. 5972656
GENERAL INFORMATION:
APPLICANT: LOPEZ, Osvaldo
APPLICANT: Wajie, Dwane E.
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STREET: 90 South 7th Street, 3100 No. 5972656west Ctr
STATE: Minneapolis
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INA PC Compatible
COMPUTER: INA PC Compatible
COMPUTER: INA PC COMPATIBLE
COMPUTER: DATENING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997
CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 17-JAN-1994
FILING DATE: 14-DEC-1992
                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 85.6%; Score 481; DB 1; L
Best Local Similarity 84.0%; Pred. No. 5.3e-38;
Matches 89; Conservative 9; Mismatches 8;
                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,864
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 919-881-3175 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-339-582-4
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-888-366-22
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MOLECULE TYPE: protein
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               ; MOLECULE TYPE
US-08-465-473B-16
                                                                                                                                                                                                                                                                                                                                                                        US-08-235-838-11
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                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                          81.9%; Score 460; DB 1; Length 637;
80.2%; Pred. No. 2.8e-35;
Live 10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/08465473B
Patent No. 5939531
GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Hardman, No. 5939531man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 RFSGSGSGRDYSFSIHNLEPEDIATYXCLHYDYLYTFGGGTKLEIK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/465,473B
FILING DATE: 5 June 1995
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
TELEGTH: 637 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4-18518/A/CIP/CONT2
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CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hesna J.
ANME: Pfeiffer, Hesna J.
A-18518/A/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOVARTIS Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (908)522 6955
NFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564 Morris Avenue
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.29
Matches 85, Conservative
                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                            linear
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ZIP: 07901-6940
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                                                                                               1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                   11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hynes, Nancy E.

APPLICANT: Hynes, Nancy E.

APPLICANT: Groner, Bernd
APPLICANT: Groner, Bernd
APPLICANT: Wickl, Markus
APPLICANT: Zwickl, Markus
APPLICANT: Zwickl, Markus
APPLICANT: Zwickl, Markus
APPLICANT: William (Growth Factor Receptor
                                                                                                                                                                                                   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                        228 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYFFGGGTKLEIK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,838
FILING DATE: TBA
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION NUMBER: GB 91-810079.3
APPLICATION NUMBER: GB 91-810079.3
APPLICATION NUMBER: GB 91-810079.3
ATTORNEX/AGENT INFORMATION:
81.9%; Score 460; DB 2;
80.2%; Pred. No. 2.8e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4-18518/A/CIP/CONT
Query Match
81.9%; Score 460; DB
Best Local Similarity 80.2%; Pred. No. 2.8e
Matches 85; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08235838 Patent No. 5571894 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 4-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wels, Winfried S. APPLICANT: Hynes, Nancy E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: CIBA-GEIGY CC
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 241 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 84; Conserv
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1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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APPLICANT: SNARY, DAVID
APPLICANT: STEWART, LORNA MD
APPLICANT: STEWART, LORNA MD
APPLICANT: YOUNG, SISSAN
APPLICANT: YOUNG, SISSAN
APPLICANT: PATES, PAUL A
TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.9%; Score 454.5; DB 2; Length 108;
83.0%; Pred. No. 1.3e-35;
ttive 8; Mismatches 9; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: January 6, 2003, 13:19:09 Job time : 9.7798 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: SADOFF, B.J.
REGISTRATION NUMBER: 3663
REFERENCE/DOCKET NUMBER: 1990-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Hukan REI light chain US-08-602-725-29
Sequence 29, Application US/08602725
Patent No. 596510
GENERAL INFORMATION:
APPLICANT: BODMER, WALTER F
APPLICANT: DURBIN, HELGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 703-816-4100 INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 83.v.
The 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: ARLINGTON STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            рp
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   137 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 196
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Batent No. 5939531

GENERAL INFORMATION

APPLICANT: Wels, Winfried S.

APPLICANT: Hynes, Nancy E.

APPLICANT: Harwerth, Ina-Maria

APPLICANT: Hardman, No. 5939531man

APPLICANT: Bardman, No. 5939531man

APPLICANT: Ardman, No. 5939531man

APPLICANT: Grover, Bernd

APPLICANT: APPLICANT: Grover, Bernd

APPLICANT: APPLICANT: Grover, Bernd

APPLICANT: APPLICANT: Grover, Bernd

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APPLICANT: APPLICANT: Grover, Bernd

APPLICANT: APPLICANT: Grover, Bernd

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEI 105
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                                                                                                                       SOFTWARES PATENTIN Release #10, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
FILING DATE: June 1995
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION NUMBER: US 07/828,832
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pfelifer, Heans J.
REGISTRATION NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (908)522 6955
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 241 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 07901-6940
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Summit
STATE: New Je
                                                                                                                                                                                                                                                                       RESULT 14
US-08-465-473B-11
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US-08-602-725-29
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January 6, 2003, 13:17:36 ; Search time 5.13939 Seconds (without alignments) 390.875 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                             562
1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published_Applications_AA:*

1: \( \cgn2_6/\text{Ptodata}/2/\text{pubpaa}/\text{VISOB_NEW_PUB.pep:*} \)

2: \( \cgn2_6/\text{Ptodata}/2/\text{pubpaa}/\text{PtoTB_PEP:*} \)

3: \( \cgn2_6/\text{Ptodata}/2/\text{pubpaa}/\text{VISOB_NEW_PUB.pep:*} \)

4: \( \cgn2_6/\text{Ptodata}/2/\text{pubpaa}/\text{VISOB_NEW_PUB.pep:*} \)

5: \( \cgn2_6/\text{Ptodata}/2/\text{pubpaa}/\text{VISO}_PUBCOMB.pep:*} \)

7: \\( \cgn2_6/\text{Ptodata}/2/\text{pubpaa}/\text{VISO}_PUBCOMB.pep:*} \)

7: \\( \cgn2_6/\text{Ptodata}/2/\text{pubpaa}/\text{VISOB_PUBCOMB.pep:*} \)

8: \\( \cgn2_6/\text{Ptodata}/2/\text{pubpaa}/\text{VISOB_PUBCOMB.pep:*} \)

10: \\( \cgn2_6/\text{Ptodata}/2/\text{Pubpaa}/\text{VISOB_PUBCOMB.pep:*} \)

11: \\( \cgn2_6/\text{Ptodata}/2/\text{Pubpaa}/\text{VISOB_PUBCOMB.pep:*} \)

11: \\\( \cgn2_6/\text{Ptodata}/2/\text{Pubpaa}/\text{VISOB_PUBCOMB.pep:*} \)

11: \\\( \cgn2_6/\text{Ptodata}/2/\text{Pubpaa}/\text{VISOB_PUBCOMB.pep:*} \)
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/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117078 seqs, 18951520 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                        US-09-155-739-7
                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                   Run on:
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## SUMMARIES

Description	Sequence 11, Appl	15.	Sequence 16, Appl	Sequence 15, Appl	Sequence 103, App	Sequence 100, App	Sequence 2, Appli		12,	9	~		4	Sequence 105, App	Sequence 7, Appli	Sequence 2, Appli	٠		_
ID	US-09-229-200A-11	US-09-229-200A-15	US-09-229-200A-16	US-09-056-160B-15	US-09-056-160B-103	US-09-056-160B-100	US-10-011-125-2	US-09-056-160B-13	US-09-056-160B-12	US-09-811-123-6	US-09-999-025-15	US-09-999-040-15	US-09-229-200A-14	US-09-056-160B-105	US-09-229-200A-7	US-10-153-159-2	US-10-153-159-16	US-09-056-160B-8	US-09-253-794-6
DB	10	10	10	10	10	10	12	10	10	10	6	6	10	10	10	6	6	10	10
Query Match Length DB	108	108	108	107	110	237	491	107	108	109	107	107	108	110	109	108	108	108	107
Query Match	85.3	85.3	83.0	80.0	79.4	79.4	79.4	79.3	79.1	79.1	78.9	78.9	78.9	78.9	78.8	78.7	78.7	78.7	78.6
Score	479.5	479.5	466.5	449.5	446.5	446.5	446.5	445.5	444.5	444.5	443.5	443.5	443.5	443.5	443	442.5	442.5	442.5	441.5
Result No.	1	7	m	4	w	9	7	ω	6	10	11	12	13	14	. 15	16	17	18	19
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85.3%; Score 479.5; DB 10; Length 108; 85.8%; Pred. No. 1e-28; Live 7; Mismatches 7; Indels 1;

Query Match
Best Local Similarity 85.89
Matches 91; Conservative

US-09-229-200A-11

TYPE: amino acid TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Sequence 4, Appli Sequence 107, App Sequence 117, App Sequence 10, Appl Sequence 2, Appli Sequence 11, Appl Sequence 11, Appl Sequence 126, Appl Sequence 13, Appli Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 19, Appli Sequence 6, Appli Sequence 6, Appli Sequence 19, Appli Sequence 19, Appli Sequence 2, Appli Sequence 2, Appli Sequence 11, Appl Sequence 111, Appl Sequence 115, Appl Sequence 6, Appli	Antibody STORAGE
0. US-10-153-159-4 0. US-09-056-160B-107 0. US-09-056-160B-107 0. US-09-056-243-73 0. US-09-940-166A-2 0. US-09-810-126 0. US-09-810-126 0. US-09-256-160B-126 0. US-09-956-087-3 0. US-00-056-160B-113 0. US-09-056-160B-113	ALIGNMENTS  229200A  al. Specific Recombinant by Johnson Plaza k  a. Johnson Plaza k  TTE, 3.5 INCH, 1.44 Mb  PC-DOS  A: US/09/229,200A  INCHOWN  I
108 1108 1109 1109 1109 1109 1109 1109 1	on US/09 79A1 iffe et 10N: CD4 NCES: 28 ADDRESS: 20 AD
7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	-200A-11  e 11, Application U  AL INFORMATION: APPLICANT: JO11iff APPLICANT: JO11iff APPLICANT: JO11iff APPLICANT: JO11iff APPLICANT: JOINIff APPLICANT: JOINIff APPLICANT: New Brun, STARET: Now Brun, STARET: NOW COMPUTE: NOW BRUN, STARET: NOW COMPUTER: IBM OPERATION NU FILING DATE: JOHN APPLICATION NU FILING DATE: JOHN REGISTRATION NU FILING DATE: JOHN APPLICATION NU FILING DATE: JOHN APPLICATION NU FILING DATE: JOHN TELECOMMUNICATION NU FILING DATE: JOHN APPLICATION NU FILING DATE: JOHN APPLICATION NU FILENT APPLICATION N
44444444444444444444444444444444444444	SGULT 1 Sequence 11, Applicati Patent No. US202009991 GENERAL INFORMATION: TITLE OF INVENT NUMBER OF SEQUE CORRESPONDENCE ADDRESSEE: STREET: ON CITY: New STRATE: NJ COUNTRY: U ZIP: 08933 COMPUTER READAB MEDIUM TYP: COMPUTER: C
01000000000000000000000000000000000000	RESULT Sequel Se

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STREET:
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                        1 DIOMIQSPSSLSASVGDRVIITCKASPDINNYLNWYQQTPGKAPKLLIXYTSTLQPGVPS 60
1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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85.3%; Score 479.5; DB 10; Length 108;
Best Local Similarity 85.8%; Pred. No. 1e-28;
Matches 91; Conservative 7; Mismatches 7; Indels 1;
                                                                                                                                                                                                                                                                                                                      APPLICANT: Joiliffe et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: JOILIFFE et al.

TITLE OF INVENTION: CD4 Specific Recombinant Antibody
CORRESPONDENCE: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYDNLIFTFGGGTKLQI 106
                                                                                                                  61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYDNLIFTFGQGTKLQI 106
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                                                                                           61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: One Johnson & Johnson Plaza CITY: New Brunswick
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STREET: One Johnson & Johnson Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
FILING DATE: 13-Jan-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: John W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: mino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-229-200A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 784-3239
TELEFAX: (908) 524-2808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-229-200A-16; Sequence 16, Application US/09229200A; Patent No. US20020099179A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                  US-09-229-200A-15; Sequence 15, Application US/09229200A; Patent No. US20020099179A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 08933-7003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                           RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 108;
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTDYTFIISSLQPEDIATYCLQQYDNLIFTFGGGTKLQI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 83.0%; Score 466.5; DB 10;
Local Similarity 84.9%; Pred. No. 8.8e-28;
No. Conservative 6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-nnc Arr. SOFTWARD:
                                                                                                                              COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: «Unknown»
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
FILLING DATE: 13-Jan-1999
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
SAPPLICANT: Baca, Manuel
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yoonne M.
ITILE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
                                                                                                                                                                                                                                                                                                              NAME: John W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 784-3239
TELEFRA: (908) 524-2808
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: South San Francisco
STATE: California
COUNTRY: USA
CITY: New Brunswick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                          COUNTRY: USA
ZIP: 08933-7003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 incl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 108
                     STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94080
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US-09-056-160B-15
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Query Match
                   Matches
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                                                                                                                                                                                                                                                                                                                                                           Score 446.5; DB 10; Length 110; Pred. No. 2.5e-26;
                                                                                                                                                                                                                                                             DB 10; Length 107;
                                                                                                                                                                                                                                                                                                8; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTDYTLTISSLQPEDFATYXCQQYSTVPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                 Pred. No. 1.5e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER RELDABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                             80.0%; Score 449.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/054,856
FILING DATE: 06-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: HASAK, JANET E.
REGISTRATION NUMBER: 28,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 103, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P1093R2
                                                      P1093R2
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Hasak, Janet E.
                                 REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
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78.58;
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STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                               79.48;
                                                                                                                                                                LENGTH: 107 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 110 amino acids TYPE: Amino Acid
                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acid
                                                                                                                                                                                                                                                                                                85; Conservative
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                                        1 DIOMIQSPSSLSASVGDRVIITCKTSQDINKYMAWYQQIPGKAPRLLIHYTSALQPGIPS 60
                                                            1 DIQLIQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS 60
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9; Mismatches 13; Indels
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                                                                                                                        61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                 Sequence 100, Application US/09056160B Patent No. US20020032315A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P1093R2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/10011125
; Patent No. US20020142388A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 100: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genentech, Inc.
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: Amino Acids
TYPE: Amino Acids
TOPOLOGY: 1:4-056.
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84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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US-09-056-160B-100
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1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                        Score 445.5; DB 10; Length
Pred. No. 2.9e-26;
9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
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COMPUTER: IMP PC COMPUTER: IMP PC COMPUTED COMPUTER: IMP PC COMPUTED                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09056160B
Patent No. USZ0020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
APPLICANT: Cowman, Henry B.
APPLICANT: Chen, Yvonne M.
TILLE OF INVENTION: ANTIBODIES
UMMBER OF SEQUENCES: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WinPatin (Generated)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P1093R2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                        Query Match 79.3%;
Best Local Similarity 78.5%;
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genentech, Inc.
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TYPE: Amino Acid
: TOPOLOGY: Linear
US-09-056-160B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hasak, Janet E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
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ZIP: 94080
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US-09-056-160B-12
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      US-09-056-160B-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 79.4%; Score 446.5; DB 12; Length 491; Best Local Similarity 78.5%; Pred. No. 8.3e-26; Matches 84; Conservative 9; Mismatches 13; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Wells, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
ITILE OF INVENTION: ANTI-VEGF ANTIBODIES
UNMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           ; | FEATURE:
; |OTHER INFORMATION: Sequence is synthesized.
US-j0-011-125-2
                    APPLICANT: Chen, Christina Yu-Ching
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1804R1
CURRENT APPLICATION NUMBER: US/10/011,125
FURENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WinPatin (Generatech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION 424
PRIOR APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P1093R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/09056160B
Patent No. US20020032315A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genentech, Inc.
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California
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Amino Acid
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; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                 LENGTH: 491
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RESULT 12
US-09-999-040-15
US-09-999-040-15
Sequence 15, Application US/0999040
Publication No. US20020193574A1
GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Armoris, William J.
APPLICANT: BATER NOTE:
CURRENT APPLICATION NUMBER: US/09/999,040
PRIOR APPLICATION NUMBER: US/09/999,040
PRIOR PLING DATE: 1094-10-31
PRIOR PLING DATE: 1998-02-18
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: US 60/030,173
PRIOR FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 33
SOUTHARE: Microsoft Word 97 SR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                         Query Match 78.9%; Score 443.5; DB 9; Length 107; Best Local Similarity 81.1%; Pred. No. 4e-26; Matches 86; Conservative 9; Mismatches 10; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jolliffe et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGRDYTFIISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTDYTFTISSLQPEDIATYXCQQYQSLPYTFGQGTKLQI 106
                                                                                                                                                                            61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI 106
                                                                                                                                                  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
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STREET: One Johnson & Johnson Plaza
CITY: New Brunswick
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; Patent No. US20020099179A1
; GENERAL INFORMATION:
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  86; Conservative
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ZIP: 08933-7003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: REI VL
; LOCATION: 1..107
US-09-999-040-15
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LENGTH: 107
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  Matches
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APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.1%; Score 444.5; DB 10; Length 109; 78.5%; Pred. No. 3.4e-26; tive 11; Mismatches 11; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 443.5; DB 9; Length 107; Pred. No. 4e-26;
                                                                                                                  APPLICANT: Sharon Erickson
APPLICANT: Sharon Erickson
APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Mark Sliwkowski
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
TITLE OF INVENTION: MATIBODY-MAYTANSINOID CONJUGATES
FILE REFERENCE: GENEWY. 073-2
CURRENT APPLICATION NUMBER: US/09/811,123
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/602,530
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Humanized Antibody Sequence US-09-811-123-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US/09/99,025
CURRENT FILING DATE: 2001-10-31
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1997-10-30
PRIOR PLICATION NUMBER: US 60/030,173
PRIOR FILING DATE: 1997-10-31
NUMBER OF SED ID NOS: 33
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/09999025 Publication No. US20020183497A1 GENERAL INFORMATION:
                                                    Sequence 6, Application US/09811123 Patent No. US20020001587A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.9%;
81.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 78.5%;
Matches 84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                   GENERAL INFORMATION:
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; LOCATION: 1..107
US-09-999-025-15
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US-09-999-025-15
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                            US-09-811-123-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIOMTOSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.9%; Score 443.5; DB 10; Length 108; 81.1%; Pred. No. 4e-26; tive 9; Mismatches 10; Indels 1;
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
FILING DATE: 13-Jan-1999
CLASSIFICATION: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                    NAME: JOHN W. WALLEN, III
RECISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
TELECOMMUNICATION INFORMATION:
TELEPHONE: (958) 784-3239
TELEFAX: (908) 524-2808
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
                                                                                                                                                                                                                                                                                                                                                                                                                           ; | SEQUENCE DESCRIPTION: SEQ ID NO: 14: US-09-229-200A-14
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APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 105, Application US/09056160B
Patent No. US20020032315Al
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                        OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: HASAK, JANEL E.
REGISTRATION NUMBER: 28,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genentech, Inc.
                                                                SOFTWARE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 108
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 18.34
Best Local Similarity 81.15
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 78.9%; Score 443.5; DB 10; Length 110; Local Similarity 77.6%; Pred. No. 4.1e-26; hes 83; Conservative 10; Mismatches 13; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.8%; Score 443; DB 10; Length 109; 76.9%; Pred. No. 4.4e-26; tive 14; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Jolliffe et al.

TITLE OF TINFUTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Johnson & Johnson
STREET: ONE Johnson & Johnson Plaza

CITY: New Brunswick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 08933-7003
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGRDYSFSISNLEPEDIATYCIQNNDLFLTTFGGGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: <URLCANDON DATA:
APPLICATION NUMBER: US/09/229,200A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: John W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 13-Jan-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (858) 784-3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09229200A Patent No. US20020099179A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (908) 524-2808
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                               ; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-160B-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 76.98
Matches 83; Conservative
                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NJ
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-229-200A-7
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                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
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Search completed: January 6, 2003, 13:29:31 Job time: 5.13939 secs

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Compugen Ltd.
GenCore version 5.1.3
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OM protein - protein search, using sw model

January 6, 2003, 13:12:26; Search time 9.85051 Seconds Run on:

(without alignments) 1034.490 Million cell updates/sec

US-09-155-739-7 Perfect score: Title:

562 1 DIQMTQSPSSLSASVGDRVT......YCLQYDNLWTFGQGTKVEIK 106 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched: 283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\* Database :

1: pir1:\* 2: pir2:\* 3: pir3:\* pir4:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	, p	۵, X		б	б	ש	kappa	kappa	light	kappa		kappa		kappa chain	kappa	kappa		lambda	kappa  hain	kappa	kappa	chai							
	ID	\$26330	S26329	C33936	809365	PH1064	PL0270	KIHURE	S52789	S26332	PL0272	E33730	PL0269	PL0271	K1HUAU	I39154	S44118	S40367	S36275	S40333	KIHULY	KIHUAG	K1HURY	S40331	S31998	S40352	S40336	K1HUSW	CD.	PC2397
	DB	7	N	7	7	7	~	Н	7	~	~	7	~	7	Н	7	~	7	7	~	Н	H	-	7	7	~	N	-	7	7
	Length	104	104	106	125	97	107	108	129	103	107	94	107	107	108	108	110	127	107	125	108	108	108	123	109	131	124	108	108	106
æ	Query Match	86.8	85.2	'n.	82.5	80.4	79.4	78.9	·	78.8		8	8	8	78.2	7.	76.4	76.4	5.		5.	74.6	74.6			ë.	ω.	З.	73.4	73.3
	Score	1	479	478	463.5	452	446.5	443.5	443.5	443	440.5	440	439.5	439.5	439.5	435.5	429.5	429.5	$\sim$			٠,	419.5			414.5	414	ë.	412.5	412
	Result No.	1	7	e	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

Ig kappa chain V r Ig kappa chain - h	Ig kappa chain pre	19 kappa chain V-I 19 kappa chain V-I	Ig kappa chain – h Iq kappa chain V-I	Ig kappa chain V-J Ig kappa chain V r	Ig kappa chain - h	Ig light chain V r Ig lambda chain V	Ig kappa chain V r	hain	hain	To kappa chain V-I
S44122 S31981	KIHUWK	KIHUAK KIHUWE	S40365 A49134	S46371 S30521	540334	PH1063 S36264	S11240	S43528	S42263	x 1 HITHII
7 7	П.		~ ~	71 7	0	~ ~	7	7	7	-
108	129	108	139	117	132	94	127	117	117	108
			72.7 139							
73.0	72.9	72.7		72.2	72.0	71.8	71.8	71.7	71.7	71 6

## ALIGNMENTS

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C;Accession: S26330
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a proteil A;Reference number: S26339; MUID:91341421; PMID:1908510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                             C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X59185; NID:952316; PIDN:CAA41895.1; PID:91334063 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F:16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 86.8%; Score 488; DB 2; Length 104; Best Local Similarity 85.6%; Pred. No. 1.6e-35; Matches 89; Conservative 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RESGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVE 104
Ig kappa chain V region - mouse
                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-104 <STA>
                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
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0y
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61 RFSGSGSGRDYSFSISNLEPEDIATYCLQYDNLWTFGGGTKLE 104 g

C,Accession: S26329
R;Stark, S.E.; Caton, A.J.
Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a proteil A;Reference number: S26309; MUID:91341421; PMID:1908510

A; Accession: S26329 A; Status: preliminary

A; Molecule type: mRNA A; Residues: 1-104 <STA>

A;Cross-references: EMBL:X59173; NID:952309; PIDN:CAA41883.1; PID:91334059 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin

F;16-90/Domain: immunoglobulin homology <IMM>

85.28; Query Match

DB 2; Length 104; Score 479:

Mon Jan

Similarity

Local

```
To kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C; Accession: PLO270
C; Accession: PLO270
S; Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J; Exp. Med: 171, 265-297, 1990
A; Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A; Reference number: PLO231; MUID:90111618; PMID:2104919
A; Residue type: mRNA
A; Residue type: mRNA
A; Residue type: mRNA
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-90/Domain: immunoglobulin homology 
C; Keywords: heterotebramer;
F; 16-90/Domain: immunoglobulin homology 
F; 24-34/Region: complementarity-determining 1
F; 16-90/Pomain: immunoglobulin homology 
                                                                                                      PHIO64

Ig light chain V region (clone 202.54) - mouse (fragment)

C; Species: Mus musculus (house mouse)

C; Date: 30-Sep-1993 #text_change 21-Jan-2000

C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C; Accession: PHIO64

R; Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J; Exp. Med. 176, 761-779, 1992

A; Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A; Reference number: PH0971; MUID: 92381444; PMID: 1512540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                        A) Experimental source: B cell, strain [NZB x NZW]F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.4%; Score 452; DB 2, 85.6%; Pred. No. 2e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F:50-56/Region: complementarity-determining 2 F:57-88/Region: framework 3 F:89-97/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                        A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 85.6
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 79.48
Matches 85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-97 <TIL>
                                                                                                                                                                                                                                                                                                                                             A; Accession: PH1064
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K1HURE
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R.Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Proc. Nati. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A.Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A.Reference number: A33936; MUID:89282831; PMID:2471975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Mus musculus (house mouse)
C; Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C; Aqcession: 809365
R; Feddersen, R:; van Ness, B.
Nucleic Acids Res. 17, 9797-9809, 1989
A; Title: Direct evidence for intrastrand DNA inversion of kappa immunoglobulin gene segm A; Reference number: 809365; MUID:90098844; PMID:2513557
A; Aqcession: 809365
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                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain V region (VM113) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
                                                           Gaps
                                                                                                1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                1 DIQMIQSPSSLSASLGGKVIITCKASQDINKYIAMYQHKPGKGPRLLIHYTSTLQPGIPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB:J04577; NID:g623187; PIDN:AAA60443.1; PID:g623189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 478; DB 2; Length 106; Pred. No. 1.2e-34; 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-125 <FED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>
84.6%; Pred. No. 9.8e-35; wismatches 7; Indels
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                                                                                                                                                                                                    61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVE 104
                                                                                                                                                                                                                               61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLE 104
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83.2%; Pred. No. 2.5e-33;
tive 7; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 85.1%; Score 478; DB
1 Similarity 83.0%; Pred. No. 1.2e
88; Conservative 10; Mismatches
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                                                   Conservative
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Matches 88; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-106 <MEE>
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                     Best Loca
Matches
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Naliternate names: 1g kappa chain V region
C; Species: Mus musculus (house mouse)
C; Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C; Accession: S26332; S26331
R; Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A; Title: Antibodies that are specific for a single amino acid interchange in a protein A; Reference number: S26332
A; Accession: S26332
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A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618; PMID:2104919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-103 <27A>>
A;Cross-references: EMBL:X59187; NID:952318; PIDN:CAA41897.1; PID:91334064
A;Note: the sequence of residues 1-8 and the corresponding nucleic acid sequence are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X59191; NID:g52321; PIDN:CAA41901.1; PID:g1334066 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <a href="https://document.com/numble/numble/">https://document.com/numble/numble/</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKL 103
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78.5%; Pred. No. 2.16
:ive 11; Mismatches
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F:50-56/Region: complementarity-determining
F:57-88/Region: framework 3
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                                                                                                                                   Ig light chain V region - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;16-90/Domain: immunoglobulin homology
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Best Local Similarity 77.74
Matches 80; Conservative
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A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
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Matches
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                                                                                                                                                                                                                                                  A.Reference number: A91663; MUID:76023758; PMID:809329
A;Accession: A91663
A;Residues: 1-108 <PAL>
A;Acterion of this chain has the Inv (1,2) marker
B;Epp. O.; Lattman, E.E.; Schiffer, M.; Huber, R.; Palm, W.
Biochemistry 14, 4943-4952, 1975
A;Title: The molecular structure of a dimer composed of the variable portions of the Ber A;Reference number: A90392; MUID:76039968; PMID:1182131
A;Contents: annotation; X-ray crystallography, 2.0 angstroms
C;Goment: This is a Bence Jones protein.
A;Gone: GB:IGKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Cross-references: GDB:136264
A; Map position: 2p12-2p12
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Saccession: 552789
C.Saccession: 552789
R.Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret, Submitted to the EMBL Data Library, March 1995
A.Bescription: Light chain V region gene usage restriction and peculiarities in myeloma-A.Reference number: 552789
                                                                                                                                                           Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
A; Title: Die Primaerstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom vollstaendige Aminosaeuresequenz des Proteins.
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                                  C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A91663; A01873
R;Palm, W.; Hilschmann, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :Cross-references: EMBL:X85995; NID:9758588; PIDN:CAA59987.1; PID:9758589; Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
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Pred. No. 1.2e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;16-90/Domain: immunoglobulin homology <IMM>F;23-88/Disulfide bonds: #status experimental
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Local Similarity 81.1%;
les 86; Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 79.4%;
Matches 85; Conservative 1
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A; Molecule type: mRNA
A; Residues: 1-129 <ROC>
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Matches
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Gaps

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Length 107;

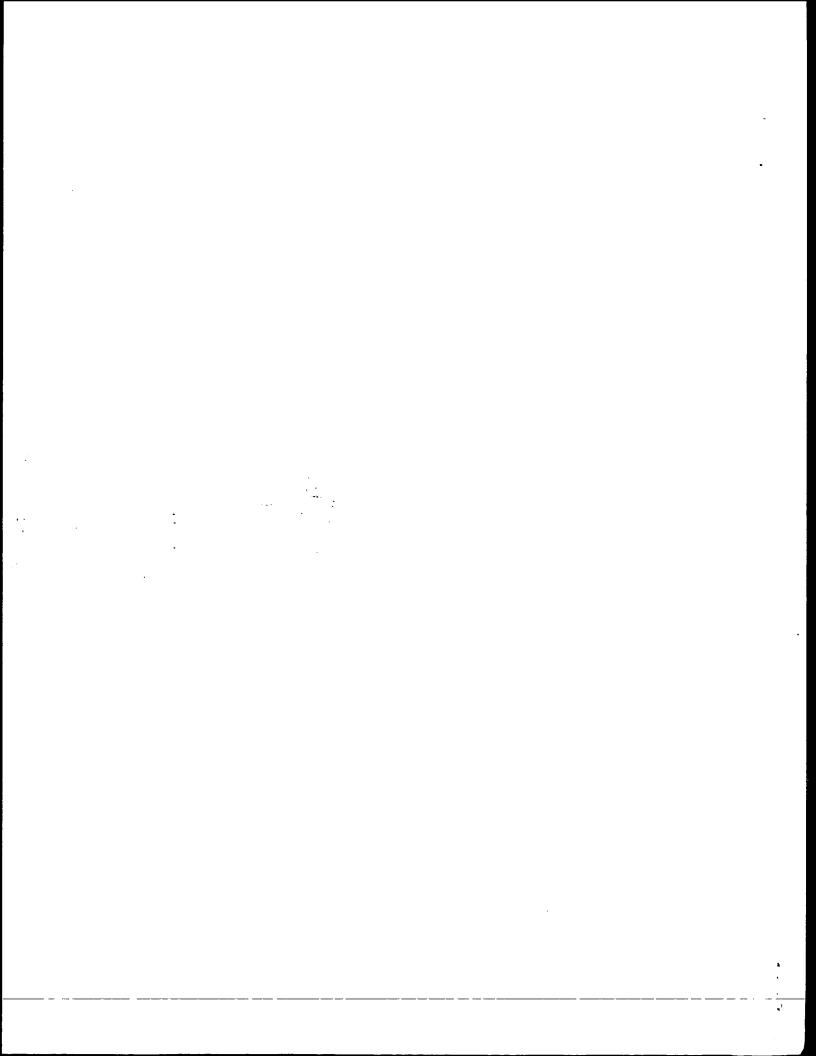
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R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A; Reference number: PLO231; MUID:90111618; PMID:2104919
A;Accession: PLO271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Molecule type: protein
A.Residues: 1-108 <SCH>
A.Note: the C region of this chain has the Inv (3) marker
B.Fehlhammer. H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; S
Biophys. Struct. Mech. 1, 139-146, 1975
Biophys. Struct. Mech. 1, 139-146, 1975
Biophys. Structure determination of the variable portion of the Bence-Jones prote
A.Fille: The structure determination of the variable portion of the Bence-Jones prote
A.Reference number: A90729; MUID: 7702243; PMID: 1234024
A.Contents: annotation; X-ray crystallography
A.Note: the structure of the V region was determined by molecular replacement methods
FEBS Lett. 222, 6-10, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds: in some cases, such as IgA and IgM, the subunits associate into
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FBBS Lett. 222, 6-10, 1987

A;Title: Chemical modification of the carboxyl groups of protein substrates enhances
A;Reference number: S02572; MUID:88005152; PMID:3115831
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000
C;Dates: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000
C;Accession: A91653; A01862; S02573
R;Schiechl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, A;Reference number: A91653; MUID:72189444; PMID:5028201
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                                                                Ig kappa chain V region (anti-DNA, 2E3VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIOMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALOPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 107;
                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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78.5%; Pred. No. 2.6e-31;
Live 10; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;50-56/Region: complementarity-determining 2 F;57-88/Region: framework 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V-I region (Au) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 78.5%
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GDB:136264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;98-107/Region: framework 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;35-49/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                                  C; Accession: PL0271
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                                                                                                                                                                                      Ig kappa chain V region (9.42) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
C;Accession: E33730
R:Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
R:Cor. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A:Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unline Reference number: A33730; MUID:89367325; PMID:2505260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: PL0269
R; Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, P. Bap, Med. 171, 265-297, 1990
A; Fitle: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A; Reference number: PL0231; MUID:90111618; PMID:2104919
A; Accession: PL0269
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C:pate: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYISTLQPGIPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:MZ6000; NID:9197119; PIDN:AAA38916.1; PID:9197120 C:Superfamilly: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 440; DB 2; Length 94
Pred. No. 2.1e-31;
7; Mismatches 6; Indels
19 kappa chain V region (anti-DNA, 3E12VK) - mouse (fragment)
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78.5%; Pred. No. 2.6e-31;
Live 10; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNL 94
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86.2%;
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Matches 81; Conservative
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A; Residues: 1-107 <SHL>
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A; Residues: 1-94 <LAW>
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Matches
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PL0269
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                                                                                                                            RESULT 11
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Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C; Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C; Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C; Date: 31-May-1996 #sequence_revision 319154
R; Schormann, N; Murrell, J.R.; Liepnieks, J.J.; Benson, M.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A; Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A proposed A; Reference number: 139154
A; Reference number: 139154
A; Mull: 9603804; PMID: 7568160
A; Accession: 139154
A; Accession: 139154
A; Accession: 139154
A; Residues: 1-108 cRES
A; Residues: 1-108 cRES
C; Superfemely: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 16-90/Domain: immunoglobulin homology <IMM>
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                                                    Gaps
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                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLESGVPS 60
                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                       ;
     Length 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 435.5; DB 2; Length 1
Pred. No. 5.8e-31;
9; Mismatches 12; Indels
Query Match 78.2%; Score 439.5; DB 1; Length Best Local Similarity 79.4%; Pred. No. 2.6e-31; Matches 85; Conservative 8; Mismatches 13; Indels
                                                                                                                                                                                                              61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain (BRE) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 79.4%;
Matches 85; Conservative
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I39154
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Search completed: January 6, 2003, 13:18:19 Job time : 9.85051 secs



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January 6, 2003, 12:48:25; Search time 5.35354 Seconds (without alignments) 821.231 Million cell updates/sec
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1 DIQMTQSPSSLSASVGDRVT......XCLQYDNLWTFGQGTKVEIK 106
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	KVIO HIMAN	KV1B HIMAN	KV1M HUMAN	KV1A HUMAN	KV1P_HUMAN	KV1Y_HUMAN	KV1Q_HUMAN	KV1W_HUMAN	KV1D_HUMAN	KV1R_HUMAN	KV1H_HUMAN	KV1F_HUMAN	KV1V_HUMAN	KV1K_HUMAN	KV1E_HUMAN	KV1L_HUMAN	KV1N_HUMAN	KV1C_HUMAN	KV1G_HUMAN	KV1X_HUMAN	KV1S_HUMAN	KV4C_HUMAN	KV5J_MOUSE	KV1J_HUMAN	KV5E_MOUSE	KV4B_HUMAN	KV50_MOUSE	KV5N_MOUSE	KV1T_HUMAN	KV11_HUMAN	KV5K_MOUSE	KV5M_MOUSE	KV5L_MOUSE
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P01613 homo sapien											
KV1U_HUMAN	KV4A_HUMAN	KV3H_HUMAN	KV3M_HUMAN	KV5T_MOUSE	KV5F_MOUSE	KV5Q_MOUSE	KV3E_HUMAN	KV5S_MOUSE	KV5U_MOUSE	KV3D_HUMAN	KV3F_HUMAN
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## ALIGNMENTS

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NCBI_TaxID=9606;
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P01605;
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Biophys. Struct. Mech. 1:139-146(1975).

-I- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF THE KAPPA CHAIN REI.

-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

HISSP; P01607; IREI.
                                                                                                                                                                     Gaps
                                                                                                                                                                                                     1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKILIYEASNLQAGVPS 60
                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILNE=72189444; PubMed=5028201;
Schiechl H., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
protein Au).";
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman B.E.,
Schwager P., Steigemann W., Schramm H.J.;
"The structure determination of the variable portion of the
                                                                                                                                               78.9%; Score 443.5; DB 1; Length 108; ilarity 81.1%; Pred. No. 4.1e-40; Conservative 9; Mismatches 10; Indels 1.
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50 52
53 54
60 61
62 67
68 69
70 75
80 82
85 90
98 98
102 106
108 AA; 11902 MW; 9E8143E1188BCEZA CRC64;
                                                                                                                                                                                                                                           61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
Imanuoglobulin V region; Bence-Jones protein.
DOMAIN
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                        108 AA
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-!- MISCELLANBOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POW V-II KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.

-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

PIR, A01871, KTHULY.

HSSP: P01607; IREI.

InterPro; IPR003596; Ig_MHC.
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                                                                                                                                                                                                          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                  1 DIOMTOSPSSLSVSVGDRVTITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Capra J.D., Klapper D.G.; Complete amino acid sequence of the variable domains of two human IgM anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                           Query Match 78.2%; Score 439.5; DB 1; Length 108; Best Local Similarity 79.4%; Pred. No. 1.1e-39; Matches 85; Conservative 8; Mismatches 13; Indels 1.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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107 FRAMEWORK-4.
88 BY SIMILARITY.
1108
11939 MW; B8011187EE6F6FB9 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Appa chain V-I region Lay.
Homo sapiens (Human).
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InterPro; IPR003596; Ig_v.
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                                                                                                                                               Titani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";
J. Biol., Chem. 244:3550/1550(1959).
-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
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                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                             74.6%; Score 419.5; DB 1; Length 108; 76.6%; Pred. No. 1.4e-37; ive 9; Mismatches 15; Indels 1
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                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
11g kappa chain V-I region Roy.
Homo Sapiens (Human).
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InterPro; IPR003596; Ig_V.
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SMART; SM00406; IGv; 1.
Immunoglobulin V region;
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HSSP; P01607; 1REI.
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                     KV1A_HUMAN
P01593;
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1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS TO 39 AND 41.
Halschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.; (In) Franck F., Shugar D. (eds.); Gamma globulins: structure and function, pp.57-74, Academic Press,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-81267384; PubMed-6167731; Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M., Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M., Popp R.A., Solomon A.; "Characterization and preliminary crystallographic data on the VL-related fragment of the human kI Bence Jones protein Wat."; J. Mol. Biol. 147:185-193(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                structural origin of altered domain interactions in immunoglobulin light-chain dimers.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95086080; PubMed=7993911;
Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M., Schomon A., Stevens F.J., Schiffer M.;
"Comparison of crystal structures of two homologous proteins:
                                                                                                                                            New York (1969).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 419.5; DB 1; Length 108;
; Pred. No. 1.4e-37;
12; Mismatches 13; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11782 MW; F5ACEDE5A313DF3A CRC64;
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                                                                                                                                                                                          MARKER.

-1. MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR, A01874, KIHURY.
INTEPPO; 1PR003006; 1g_MHC.
InterPro; 1PR003596; 1g_V.
Pfan; PF00047; 1g; 1.
SWART: SW00406; 1Gv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAMEWORK-1
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75.78;
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InterPro; IPR003006; Ig_MHC.
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Homo sapiens (Human).
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129
129 AA;
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                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                     KV1W_HUMAN
P04431;
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SEQUENCE
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"The primary structure of a human immunoglobulin L-chain of kappa-type (Bence-Jones protein Scw.), II: The chymotryptic peptides and the complete amino acid sequence."
HOPPE-Seyler's Z. Physiol. Chem. 355:842-866(1974).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.6%; Score 413.5; DB 1; Length 108; 74.8%; Pred. No. 6.1e-37; ive 10; Mismatches 16; Indels 1.
                                                                                                                                                               Score 419.5; DB 1; Length 108; Pred. No. 1.4e-37;
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Bence-Jones protein; 3D-structure.
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COMPLEMENTARITY-DETERMINING-1.
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                                         COMPLEMENTARITY - DETERMINING - 1.
                                                                 COMPLEMENTARITY - DETERMINING-2.
                                                                                       COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                      11; Mismatches 14; Indels
                                                                                                                                                                                                                                                        61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                  61 RFSGSGSGTDFTFTISSLQPEDIATYCQQYDTLPLFFGGGTKVDIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11764 MW; 32CECDDDF9644414 CRC64;
                                                                                                                                            11737 MW; D9D941B3F0FAE697 CRC64;
                                                                                                            BY SIMILARITY.
TN -> SD (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin V region; Bence-Jones protein.
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                                                                                                    FRAMEWORK-4.
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                                                                            FRAMEWORK-3
                                 FRAMEWORK-1
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InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
                                                                                                                                                                 74.6%;
75.7%;
                                                                                                                                                                                        81; Conservative
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SM00406; IGv; 1.
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HSSP; P01607; 1REI.
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Best Local Similarity
                                                                                                                                            108 AA;
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                                                                                                                                                                             Best Local Similarity
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P01609;
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DISULFID
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outsation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                      1 DIOMIQSPSSLSASVGDRVIITCQASQDIRKHLNWYDQRPGRAPRLLIYGASTLETGVPS 60
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1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLIKE-85014148; PubMed-6091049; Klobeck H.G., Combriato G., Zachau H.G.; Klobeck H.G., Combriato G., Zachau H.G.; Intunuoglobulin genes of the Kappa light chain type from two human lymphoid cell lines are closely related."; Nucleic Acids Res. 12:6995-7006(1984).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                 RESGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Walker precursor.
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74.8%; Pred. No. 2e-36;
iive 10; Mismatches
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PIR; A01883; K1HUWK.
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SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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KV1D\_HUMAN

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NCBI_TaxID=9606;
          [mmunoglobulin
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SMART; SM0040
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P01600;
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-1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUYYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIQMIQSPSTLSASVGDRVAITCRASQNISSWLAWYQQKPGKAPKVLIYKSSSLESGVPS 60
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                                                                                                                                                                                                                                                                                                                                                              -1- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN. PRISP, 801664; KIHUAR. HSSP. P80362; IMTL. INTERPROT IPRO3006; Ig_MHC.
                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goni F., Frangione B., "Amino acid sequence of the Fv region of a human monoclonal IgM (protein WEA) with antibody activity against 3,4-pyruvylated galactose in Klebsiella polysaccharides K30 and K33.";
                                                                                                                                                                                                                                                                                                          Eur. J. Biochem. 49:377-391(1974).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                                                                                                   Milstein C.P., Deverson E.V.;
"Primary structure of kappa light chain from a human myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 AA; 11703 MW; EIBFODF9844C3346 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 72.8%; Score 409; DB 1;
Local Similarity 68.9%; Pred. No. 1.8e-36;
nes 73; Conservative 20; Mismatches 13.
                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region CAR.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region WEA.
    107 AA
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INTERPO: IPR003006; Ig_MHC.
INTERPO: IPR003596; Ig_v.
Pfam; PF00047; Ig; I.
SWART; SW00406; IGv; I.
    STANDARD;
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KV1D_HUMAN
P01596;
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HOPPE-SEVIER'S Z. Physiol. Chem. 351:1291-1295(1970).
-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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"The primary structure of a monoclonal kappa-type immunoglobulin L-
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                              72.7%; Score 408.5; DB 1; Length 108; 72.0%; Pred. No. 2e-36;
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                                        COMPLEMENTARITY - DETERMINING - 1.
                                                                               COMPLEMENTARITY - DETERMINING - 2.
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                                                                                                                                                                                                                                                                                      17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                  11840 MW; 9249B61F0945618C CRC64;
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15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Hau.
region; Monoclonal antibody. 23 FRAMEWORK-1.
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21-JUL-1986 (Rel. 01, Last seq
15-JUL-1999 (Rel. 38, Last anno
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HSSP; P80362; IWTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
                                                                                                                                                                                                                                                                                    77; Conservative
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                                                                                                                                                                                                     108 AA;
                                                                                                                                                                                                                                                                 Local Similarity
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Best Local Similarity
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"Comparative structural studies on the light chains of human immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker."; J. Biochem. 77:127-1296(1975).

-! MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-! MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Ka.
10 kappa chain V-I region Ka.
11 kappa chain V-I region Ka.
12 kappa chain V-I region Ka.
13 kappa chain V-I region Ka.
14 kappa chain V-I region Ka.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                        MEDLINE=86174817; PubMed=3083240;
MEDLINE=86174817; PubMed=3083240;
MUDULET F.E., O'Connor T.P., Benson M.D.;
Polymcraphism in a Kappa I primary (AL) amyloid protein (BAN).";
MOI. Immunol. 23:73-78(1986).
PIR; A01878; KIHUBN.
PIRSP; PRO30362; IMTL.
InterPro; IPR003065; Ig_MHC.
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COMPLEMENTARITY-DETERMINING-2.
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HSSP; P80362; LWTL.
INCAPPO: IPRO03006; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfam; PF00047; Ig; Ig_U.
Immunoglobulin V region; Bence-Jones protein.
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SMART; SM00406; IGv; 1.
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                                                   NCBI_TaxID=9606;
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"The covalent structure of a human gamma G-immunoglobulin. X.

"The covalent structure of a human gamma G-immunoglobulin. X.

"The covalent structure of a human gamma G-immunoglobulin. X.

"Interportation of the covalent                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-71064023; PubMed-5489770;
Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VI. Amino
acid sequence of the light chain.";
Biochemistry 9:3155-3161(1970).
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                                                                                                                                                                                                                                                                                                       Ig kappa chain V-I region EU.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Indels
     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
                                61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQNYITPTSFGQGTRVEIK 107
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13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Appa chain V-I region BAN.
Homo sapiens (Human).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                    108 AA
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MEDLINE=71064027; PubMed=4923144;
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70.1%;
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P04430;
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P01598;
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Milstein C.P., Deverson E.V.;
The amino acid sequence of a human kappa light chain.";
The amino acid sequence of a human kappa light chain.";
Blochem. J. 123:945-958(1971).
C. -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER. RISP, PO1667; IREI.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003966; Ig_V.
R Pfam; PF00047; ig; 1.
N Mimunoglobulin V region.
The DOMAIN 1 23 COMPLEMENTARITY-DETERMINING-1.
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The DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                         Homo sapiens (Human).
Washaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                             DB 1; Length 108;
   COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.
BY SIMILARITY.
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97 C.C. FRAMEWORK-4.
107 FRAMEWORK-4.
88 BY SIMILARITY.
108
AA, 11900 MW; 768839FBED5A2F4B CRC64;
                                                                           69.5%; Score 390.5; DB 1; Length 66.4%; Pred. No. 1.6e-34; Live 19; Mismatches 16; Indels
                                                                                                                                                                           23 FRAMEMORK-1.
34 COMPLEMENTARITY-DETERMINING-
49 FRAMEMORK-2.
56 COMPLEMENTARITY-DETERMINING-
88 FRAMEMORK-3.
97 COMPLEMENTARITY-DETERMINING-
107 FRAMEMORK-4.
108 BY SIMILARITY.
108 BY SIMILARITY.
11661 MW; BDD6E350017F1E51 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region DEE.
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                                                                                       Local Similarity 66.4%
nes 71; Conservative
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Best Local Similarity
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P01597;
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1 DIQMTQSPRSSLSASVGDRVT......YCLQYDNLWTFGQGTKVEIK 106
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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Description	Ogul77 homo sapien			Ogul70 homo sapien	Ogul81 homo sapien	Ogul79 homo sapien	O9r1a5 musculu			O96pf6 homo sapien						
ID	Q9UL77	Q921A6	Q96SA9	09UL70	Q9UL81	09UL79	Q9R1A5	091WS9	Q8R062	Q96PF6	Q9JL84	Q91WF8	Q920E6	O9OYF0	09UL83	08VCP0
DB	4	11	4	4	4	4	11	11	11	4	11	11	11	11	4	11
% Query Aatch Length DB	108	241	107	108	107	.108	214	233	234	116	107	234	109	298	108	234
& Query Match	76.2	74.4	73.7	72.3	70.3	9.89	68.4	67.5	65.7	65.0	64.5	63.3	62.9	60.1	59.9	.59.7
Score	428.5	418	414	406.5	395	385.5	384.5	379.5	369.5	365.5	362.5	355.5	353.5	337.5	336.5	335.5
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Q9u186 homo sapien Q9u178 homo sapien Q9u186 homo sapien Q91589 mus musculu Q8v190 mus musculu Q8v190 mus musculu Q9u174 mus musculu Q9u174 mus musculu Q9u174 mus musculu Q9u174 mus musculu Q9u178 mus musculu Q9u178 mus musculu Q9u176 mus musculu Q8vci6 homo sapien Q8wuk4 homo sapien Q8wuk4 homo sapien Q9u182 homo sapien	108 AA. ence update) tation update) chain variable region a; Vertebrata; Euteleostomi; ini; Hominidae; Homo.	NE-98277139; PubMed-9614934; Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., In reactive autoantibodies in rheumatic carditis and normal "" Immunol. Immunopathol. 87:184-192(1998). FO15035037; AAD56273.1; PRO5 IPRO30306; Ig_MHC. PRO5 IPRO30306; Ig_MHC. PRO6047; ig; 1. SM00406; IGv; 1. ER 108 NCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64; ACE 108 AA; 11738 MW; C06681716C4D16F3 CRC64; ACE 108 AB; In Mismatches 16; Indels 1; Gaps 1; BI SIMILARITY 76.6%; Pred. No. 5.4e-41; B2; CONSETVATITCKTSODINKYMAWYOOTPGKAPRILIHYTSALQPGIPS 60	9
4 09UL85 4 09UL78 4 09UL78 10 09J589 111 08VL70 110 08RC28 111 09ERZ9 111 09SEZ9 111 09JL74 111 09JL74 111 09JL78 111 09JL78 111 09JL78 111 09JL78 111 09JL78 111 09JL78 111 09JL78 111 09JL78 111 09JL80 111 09J	PRT; 1 Created) Last seque Last annot in light c ; Craniata ; Catarrhi	de=9614934; Merwe P.L., Kalis tibodies in rheuma tthol. 87:184-192(1 3.1;WHCV. 38 MW; C06681716C 38 MW; C06681716C .2%; Score 428.5; .6%; Pred. No. 5. e 8; Mismatche NTITCKTSQDINKYMAWY.	ITCRASQSISSYL
59.1 58.9 58.9 57.4 57.4 57.4 55.8 55.8 55.2 50.3 50.5 50.5 50.5 50.5 60.5	N TITE RE	TRE=98277139; PubMed=9614  'Liu B., Van der Merwe in Dective autoantibodi s, ', Immunol. Immunopathol. IMMUNOL. IREI. PRO136037; AAD56273.1; - PRO13605; IREI. PRO1360596; Ig_V. PRO017; IG; I. PRO019596; Ig_V. PRO017; IG; I. FER 108 108 SNCE 108 AA; 11738 MW; ACE 108 AA; 11738 MW; ACE 108 AA; 11738 MW; ACC 108 AA; 11778 MW; ACC 108 AA; 11778 MW; ACC 108 AA; 11776 MG; ACC 108 ACC 108 MG; A	
117 332 118 331 119 332 120 322.5 22 313.5 22 313.5 22 306.5 22 306.5 22 20.5 306.5	T 1 29UL/77 20UL/77	MEDLINE=98277139; Wu X., Liu B., Van Young D.C.; "Myosin reactive a fetus."; Clin. Immunol. Imm EMBL; AF035037; AR HSSP; P01607; 1RE1 InterPro; IPR00350 INTERPRO; IP	
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                 # Ouery Match
Best Local Similarity
    Matches 80; Conserv
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Q9UL70
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EMBL: U88067; AB48044.1; --
InterPro: IPR003006; Ig_MHC.
PÉam: PF00047; Ig: 2.
NON_TER
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
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MEDLINE-98375893; PubMed-9712075;
MEDLINE-98375893; PubMed-9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
EMBL: U96396; AAB68785.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.4%; Score 418; DB 11; Length 241; 73.6%; Pred. No. 2.2e-39; tive 12; Mismatches 16; Indels (
61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
                        61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 AA; 26086 MW; 0276887248E9C771 CRC64;
                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 20, Last annotation updat
Anti-CEA 79 single chain FV fragment (Fragment).
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                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78; Conservative
                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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SEQUENCE
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                                                                                                                                                                                    Q921A6;
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                                                                                                                RESULT 2
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1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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     Length 107;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                       17; Indels
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                                                                                                                                                                                                                 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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73.7%; Score 414; DB 4;
illarity 75.5%; Pred. No. 2.4e-39;
Conservative 9; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035044; AAD56280.1; -.
HSSP; P01607; IRRI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00356; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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MEDLINE=98277139; PubMed=9614934;
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Best Local Similarity 72.9%
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                     Homo sapiéns (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                           Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 385.5; DB 4; Length 108;
Pred. No. 4.1e-36;
8; Mismatches 21; Indels 1.
        Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                               Query Match 70.3%; Score 395; DB 4; Length 107; Best Local Similarity 71.7%; Pred. No. 3.4e-37; Matches 76; Conservative 10; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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                                                                                                                              107 AA; 11501 MW; 070549FDE0754748 CRC64;
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EMBL; AP035035; AAD56271.1; -.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                           MEDLINE=98277139; PubMed=9614934;
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11787 MW;
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72.0%;
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SMART; SM00406; IGV; 1.
                                                                                                                      107
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        Wu X., Liu
Young D.C.;
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                                      fetus.";
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                                                                                                                                                                                                                                                                           Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF15.371; AAD40.242.1;
HISSP; D01679; ZFBJ.
InterPro; IPR003006; Ig_AHC.
InterPro; IPR003506; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Kappa light chain of Mab7 (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.4%; Score 384.5; DB 11; Length 66.4%; Pred. No. 1.2e-35; vative 18; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL: BC013496; AAH13496.1; -InterPror: IPR03065; Ig_MHC. Pfam: PF00047; 19: 2. PROSITE; PS00299; IG_MHC; UNKNOWN_1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.8 kDa protein (Fragment).
  214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 2.
SMART; SMO406; igy; 1.
SMART; SM00410; ig_like; 1.
PROSITE; PS00290; ig_MHC; UNKNOWN_1.
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Best Local Similarity 66...
And 71; Conservative
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PRELIMINARY;
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                                                                                                                                                                                                                NCBI_TaxID=10090;
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SEQUENCE
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Q9R1A5
Q9R1A5;
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Q91WS9;
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MEDLINE=20448942; PubMed=10992488;
            71; Conservative
                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                           STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=COLON;
                                                                                                                                                                                                                                                                   (Fragment).
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NON_TER
SEQUENCE
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                                                                                                                                                                                   09JL84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
Matches
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Q9JL84
            Matches
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                       20 DIQMIQITSSLSASLGDRVIISCSGSGGIANYLNWYQQKPDGIVKLLIYYISSLHSGVPS 79
         DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21361171; PubMed=11468171; Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.; The tropism of organ involvement in primary systemic amyloidosis: contributions of Ig V(L) germ line gene use and clonal plasma cell
                                                                                                                                                                                                                       Hypothetical 25.9 kDa protein.
Was musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                          65.7%; Score 369.5; DB 11; Length 234; 66.4%; Pred. No. 6.9e-34; ive 14; Mismatches 21; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 116;
                                                            61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC027418; AAH27418.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                   234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 AA; 12735 MW; E796FC2217BFCF57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Kappa 1 light chain variable region (Fragment).
SDNRI.
                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 AA.
                                                                                                                                                          234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 365.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blood 98:714-720(2001).
EMBL; AF361758; AAK51465.1; -.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      71; Conservative
                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                           Qu'ery Match
Bést Local Similarity
Mátches 71; Conserv
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                   TISSUE=COLON;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Q96PF6
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Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin. Infect. Immun. 68:5803-5808(2000).
EMBL: AF206022; AAF69320.1; -.
HSSP: P80362; IMTL.
InterPro; IPR003096; Ig_MHC.
                                     1; Gaps
                                                                                                1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                           1 DIOMTOSPSSLSASVGDRVTFICOASQDIANHLNWYQKKPGEAPKFLIYDGSFLKTGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 64.5%; Score 362.5; DB 11; Length Local Similarity 65.4%; Pred. No. 1.7e-33; nes 70; Conservative 11; Mismatches 25; Indels
66.4%; Pred. No. 8.4e-34;
tive 14; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                  61 RFSGGGSAINFIVIISSLQPEDFAIYYCQQYHHLPFTFGPGTKVDFK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGRDYTFIISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel.) 19, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 107 107 108 MW; ACF9B1253ACA1E5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25-9 kba protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 AA.
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1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                     Shinohara N., Demura T., Fukuda H.; Isolation of a vascular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phage display subtraction method.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.1%; Score 337.5; DB 11; Length 298; 58.9%; Pred. No. 3.9e-30; Live 19; Mismatches 24; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.9%; Score 336.5; DB 4; Length 108; 60.2%; Pred. No. 1.5e-30; 1.ve 17; Mismatches 23; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGRDYTFIISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK 279
                                                                                                                                                                                                                                                                                                                                                                                                           298 AA; 31867 MW; E0F96B8A17004317 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;
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EMBL; AB036341; BAA88633.1; -.
HSSP; P01607; IREI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035031; AAD56267.1; -.
HSSP; P80362; IWTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY 2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last seq 01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                               MEDLINE-20183931; PubMed-10706631;
                                                         SEQUENCE FROM N.A. SEQUENCE SPLEEN; "NAIR/C; TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                             InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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InterPro; IPR003006; Ig_MC.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
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Matches 63; Conservative
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                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 2.
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                                      NCBI_TaxID=10090;
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SEQUENCE
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                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                              21 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLYLGVPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.; "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalla, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CN 8 scFv.
CN 8
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                         DB 11; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.9%; Score 353.5; DB 11; Length 109; 61.7%; Pred. No. 1.8e-32; Live 16; Mismatches 24; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TremBLrel. 19, Last sequence update)
01-MAR-2002 (TrEmBLrel. 20, Last annotation update)
Pterin-mimicking anti-idiotope kappa chain variable region
                                                                                                                                                                                                                                Query Match 63.3%; Score 355.5; DB 11; Length Best Local Similarity 64.5%; Pred. No. 2.7e-32; Matches 69; Conservative 17; Mismatches 20; Indels
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC015292; AAH15292.1; ... InterPro; IPR003006; Ig_MHC. InterPro; IPR001805; Ribosomal_S2. PROSTTE; PS00290; IG_MHC; UNKNOWN_1. PROSTTE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307938; AAL09422.1; ...
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                               1 protein.
234 AA; 25929 MW; BODOBOE6EB7812D2 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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